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SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB# 71349

Requester's Full Name: Dan Lin Examiner #: 69507 Date: 7-18-02
 Art Unit: 1646 Phone Number 30 8-4008 Serial Number: 09/698419
 Mail Box and Bldg/Room Location: CMI 6B02 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*please search SEQ ID NO: 14
 of 09/698419.*

Edward Hart
 Technical Info. Specialist
 STIC/Biotech
 CMI 6B02 Tel: 305-9203

10 COI

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____

NA Sequence (#) _____

STN _____

Searcher Phone #: _____

AA Sequence (#) _____

Dialog _____

Searcher Location: _____

Structure (#) _____

Questel/Orbit _____

Riblinoranic

Dr.Link _____

7/19/02

prot. 14

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2002, 14:36:59 ; Search time 13.07 Seconds
(without alignments)
691.467 Million cell updates/sec

Title: US-09-698-419-14
Perfect score: 1963
Sequence: 1 MANYSHADNIDLWLSPLFA.....STLLYCKRSLRPREPCVY 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2.6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2.6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2.6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2.6/ptodata/2/1aa/PCRTUS.COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1 | 1963 | 100.0 | 370 | 3 | US-09-251-373-2 Sequence 2, Appl1 |
| 2 | 264.5 | 13.5 | 478 | 3 | US-09-292-071-31 Sequence 31, Appl1 |
| 3 | 264.5 | 13.5 | 478 | 4 | US-09-292-069A-31 Sequence 31, Appl1 |
| 4 | 258 | 13.1 | 470 | 4 | US-09-292-071-25 Sequence 25, Appl1 |
| 5 | 258 | 13.1 | 470 | 4 | US-09-292-069A-25 Sequence 25, Appl1 |
| 6 | 257.5 | 13.1 | 453 | 1 | US-08-570-157-7 Sequence 7, Appl1 |
| 7 | 256.5 | 13.1 | 478 | 3 | US-09-292-071-33 Sequence 33, Appl1 |
| 8 | 256.5 | 13.1 | 478 | 4 | US-09-292-069A-33 Sequence 33, Appl1 |
| 9 | 255 | 13.0 | 330 | 1 | US-08-118-270-19 Sequence 19, Appl1 |
| 10 | 255 | 13.0 | 330 | 5 | PCR-US93-08528-19 Sequence 19, Appl1 |
| 11 | 253.5 | 12.9 | 471 | 1 | US-07-817-920-8 Sequence 8, Appl1 |
| 12 | 253.5 | 12.9 | 471 | 1 | US-08-370-542-7 Sequence 7, Appl1 |
| 13 | 253.5 | 12.9 | 471 | 1 | US-08-117-006-8 Sequence 8, Appl1 |
| 14 | 253.5 | 12.9 | 471 | 1 | US-08-216-594-8 Sequence 8, Appl1 |
| 15 | 253.5 | 12.9 | 471 | 1 | US-08-542-358-7 Sequence 7, Appl1 |
| 16 | 253.5 | 12.9 | 471 | 2 | US-08-244-434-2 Sequence 2, Appl1 |
| 17 | 253.5 | 12.9 | 471 | 2 | US-09-018-351-7 Sequence 8, Appl1 |
| 18 | 253.5 | 12.9 | 471 | 4 | PCR-US93-00149-8 Sequence 8, Appl1 |
| 19 | 253.5 | 12.9 | 471 | 5 | US-08-570-157-3 Sequence 3, Appl1 |
| 20 | 253 | 12.9 | 448 | 1 | US-09-032-742-11 Sequence 11, Appl1 |
| 21 | 251 | 12.8 | 471 | 4 | US-07-996-772A-11 Sequence 11, Appl1 |
| 22 | 250 | 12.7 | 471 | 4 | US-09-032-742-11 Sequence 11, Appl1 |
| 23 | 250 | 12.7 | 471 | 4 | US-09-032-742-11 Sequence 11, Appl1 |
| 24 | 250 | 12.7 | 471 | 4 | US-09-032-742-11 Sequence 11, Appl1 |
| 25 | 250 | 12.7 | 471 | 4 | US-09-032-742-11 Sequence 11, Appl1 |
| 26 | 248.5 | 12.7 | 357 | 1 | US-08-356-405-2 Sequence 2, Appl1 |
| 27 | 247.5 | 12.6 | 447 | 1 | US-07-937-603-29 Sequence 29, Appl1 |

| | | | | | |
|----|-------|------|-----|---|--------------------------------------|
| 28 | 247.5 | 12.6 | 447 | 1 | US-07-978-892A-6 Sequence 6, Appl1 |
| 29 | 247.5 | 12.6 | 447 | 4 | US-08-029-170-29 Sequence 29, Appl1 |
| 30 | 243.5 | 12.4 | 388 | 5 | US-08-446-822-8 Sequence 8, Appl1 |
| 31 | 243.5 | 12.4 | 388 | 5 | US-08-446-822-8 Sequence 8, Appl1 |
| 32 | 243 | 12.4 | 353 | 2 | US-08-467-559B-10 Sequence 10, Appl1 |
| 33 | 243 | 12.4 | 452 | 1 | US-07-937-609-16 Sequence 16, Appl1 |
| 34 | 243 | 12.4 | 452 | 2 | US-08-029-170-16 Sequence 16, Appl1 |
| 35 | 242.5 | 12.4 | 357 | 2 | US-08-031-538-4 Sequence 4, Appl1 |
| 36 | 241.5 | 12.3 | 460 | 1 | US-07-817-920-4 Sequence 4, Appl1 |
| 37 | 241.5 | 12.3 | 460 | 1 | US-07-996-772A-9 Sequence 9, Appl1 |
| 38 | 241.5 | 12.3 | 460 | 1 | US-08-370-542-4 Sequence 4, Appl1 |
| 39 | 241.5 | 12.3 | 460 | 1 | US-08-117-006-4 Sequence 4, Appl1 |
| 40 | 241.5 | 12.3 | 460 | 1 | US-08-216-594-4 Sequence 4, Appl1 |
| 41 | 241.5 | 12.3 | 460 | 1 | US-08-342-358-4 Sequence 4, Appl1 |
| 42 | 241.5 | 12.3 | 460 | 3 | US-09-018-351-4 Sequence 4, Appl1 |
| 43 | 241.5 | 12.3 | 460 | 4 | US-09-032-742-4 Sequence 4, Appl1 |
| 44 | 241.5 | 12.3 | 460 | 5 | PCR-US93-00149-4 Sequence 4, Appl1 |
| 45 | 241 | 12.3 | 458 | 1 | US-08-310-271-2 Sequence 2, Appl1 |

ALIGNMENTS

RESULT 1
Sequence 2 Application US/09251373
Patent No. 6071722
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
APPLICANT: ELSHOUBABY, NABIL
TITLE OF INVENTION: A G-PROTEIN COUPLED 7TM RECEPTOR
TITLE OF INVENTION: (AXOR-1)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,373
FILING DATE: 16-FEB-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/082,981
FILING DATE: 24-APR-1998
APPLICATION NUMBER: 60/089,639
FILING DATE: 17-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-251-373-2

Query Match 100.0%; Score 1963; DB 3; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4,4e-169;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNTSPITAFIKTSLGFIIGSVGNLLISLLVKDKTLHRAPIYFLL 60
 DB 1 MANYSHADNIIQNTSPITAFIKTSLGFIIGSVGNLLISLLVKDKTLHRAPIYFLL 60
 QY 61 DLCCSDILRSACFPFVENSNGSTWYGTLLCKVIAELGVLSCHPTAFMLFCISVTRY 120
 DB 61 DLCCSDILRSACFPFVENSNGSTWYGTLLCKVIAELGVLSCHPTAFMLFCISVTRY 120
 QY 121 LAIAHREYTKLTFTWTCIAVICMWTLSVAAFPVLDVGYSFIREDOCTFOHRSR 180
 DB 121 LAIAHREYTKLTFTWTCIAVICMWTLSVAAFPVLDVGYSFIREDOCTFOHRSR 180
 QY 181 ANDSGFMILLIILATOLVTLKLFYHDKRKKMPVOFVAASQNTFHHGASGQA 240
 DB 181 ANDSGFMILLIILATOLVTLKLFYHDKRKKMPVOFVAASQNTFHHGASGQA 240
 QY 241 ANWLAGFGGPTPTLLGIRONANTGRRLLVLDEFKMEKRISRMFYIMTFELTLMGP 300
 DB 241 ANWLAGFGGPTPTLLGIRONANTGRRLLVLDEFKMEKRISRMFYIMTFELTLMGP 300
 QY 301 YLVACYWRFAGPYPGGFLTAAYMASPAQAGINPVCIFSRRELRCESTLLTCRKS 360
 DB 301 YLVACYWRFAGPYPGGFLTAAYMASPAQAGINPVCIFSRRELRCESTLLTCRKS 360
 QY 361 RLREPYCVI 370
 DB 361 RLREPYCVI 370

RESULT 2

US-09-292-071-31
 ; Sequence 31, Application US/09292071
 ; Patent No. 6107324

GENERAL INFORMATION:

APPLICANT: Behan, Dominic
 APPLICANT: Chalmers, Derek
 TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
 TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arena Pharmaceuticals, Inc.
 STREET: 6166 Nancy Ridge Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA

ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/292,071
 FILING DATE: April 14, 1999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Rosen
 REGISTRATION NUMBER: 39,822
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 564-6525
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 478 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-09-292-071-31

Query Match 13.5%; Score 264.5; DB 3; Length 478;
 Best Local Similarity 23.9%; Pred. No. 3.6e-16;
 Matches 83; Conservative 61; Mismatches 153; Indels 51; Gaps 9;

QY 30 IIGSVGNLLISLLVKDKTLHRAPIYFLLDCCSDILRSACFPFVENSNGSTWY 89
 DB 84 VILITAGNLVIMASLEKRLONATNYFLMSLAIDMLGFLVMPVSMILTYGYMPL 143
 QY 90 GTLLCKVIAELGVLSCHPTAFMLFCISVTRYLAIA---HHREYTKLTFTWTCIAVICM 145
 DB 144 PSKLCANWYILDVLFSTASIMHLCAISLDRYVAQNIHHSRFSRKAFILKIA---V 199
 QY 146 WTLVSMAFP-PVLDVGYSFIREDOCTFOHNSFRANDSLGFMILLIILATOLVYLK 204
 DB 200 WTLVSIGSMIPVFGIADDKSKVEKGLADDFVIGSFVSFFILTIWITYFLTIK 259
 QY 205 L-----IFFYHDKRKKMP---VOFVAASQNTFHHGASGQAANWLAGFGGPTPTL 256
 DB 260 VLRRQALMLHGTETPEPPGLSLDFLKCKCRN-----TAEBENSAN----- 299
 QY 257 LGIRONANTGRRRL-----VLDEFKMEKRISRMFYIMTFELTLMGPVACYWRY 309
 DB 300 ----PNDQARRKKRKRPRGTMQAINNERKSKVLGIVFLFYVMWCPFTITINAV 355
 QY 310 FAR---GPVPGGFLTAAYMASPAQAGINPVCIFSRRELRCESTLL 354
 DB 356 ICKESCNEVDIYALNFWVIGYLSAVNPVLYTLFKIYRARSNTL 403

RESULT 3

US-09-292-069A-31
 ; Sequence 31, Application US/09292069A
 ; Patent No. 6140509

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P
 APPLICANT: Chalmers, Derek T
 APPLICANT: Foster, Richard J
 APPLICANT: Glen, Robert C
 APPLICANT: Lawless, Michael S
 APPLICANT: Liaw, Chen W
 APPLICANT: Liu, Qian
 APPLICANT: Russo, Joseph F
 APPLICANT: Smith, Julian R
 APPLICANT: Thomsen, William J
 TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
 TITLE OF INVENTION: Serotonin Receptors and Small Molecule Modulators
 TITLE OF INVENTION: Thereof
 FILE REFERENCE: AREN0033
 CURRENT APPLICATION NUMBER: US/09/292,069A
 CURRENT FILING DATE: 1999-04-14
 PRIOR APPLICATION NUMBER: 60/090,783
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/112,909
 PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 60/123,000
 PRIOR FILING DATE: 1999-03-05
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 31
 LENGTH: 478
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: No. 6140509e1
 OTHER INFORMATION: Sequence
 US-09-292-069A-31

Query Match 13.5%; Score 264.5; DB 4; Length 478;
 Best Local Similarity 23.9%; Pred. No. 3.6e-16;
 Matches 83; Conservative 61; Mismatches 153; Indels 51; Gaps 9;

QY 30 IIGSVVGNLLISILYKDKTLHRAVYFLLDCCSDLSAICFPFVNSVKNSTWY 89
 DB 84 VILLITAGNLTMAVSLKELONATYFLMSLAIDMLGFLVMPVSMITLYGRMPL 143
 QY 90 GLTYKVIATFLVGLSCFHTAFMLFCISVTRYLAIA-----HHREYTKRLTFWTCIAICMV 145
 DB 144 PSKLCVAVIYLDVLESTASIMHLCALSLDRVAIQNPISHSRFSKRAFLKITA-----V 199
 QY 146 WFLSVMAFP-PVLDVGYTSFIREDOCTQHSFRANDSLGEMLLALILATOLVYLK 204
 DB 200 WITISVIGSMIPVGLDODDSKVEKSGCLLADNDFVLIGSFVSFPIITLIMVITYFLIK 259
 QY 205 L-----IFVHBRKMKP---VOPVAVSONMTFHGASGQAANLACGRCPTPTL 256
 DB 260 VLRQALMLHGTPEPPGISLDFLCKCKRN-----TAEENSAN----- 299
 QY 257 LGIRONANTGRRRL-----VLDEFKMEKRISRMFYMTFLFLMGPIYACVYRV 309
 DB 300 ---PQODONARRKKRRPRCTMOAINNERKASKVLGIVFLELVMMCPFITINMAV 355
 QY 310 FAR---GPVPPGFLTAAVWMSFAOGINPFVCIFSNRELRCPSTL 354
 DB 356 ICKESCNEVIGALLNVFWIGILSSAVNPVYTLTKITRRASNTL 403

RESULT 4

US-09-292-071-25
 ; Sequence 25, Application US/09292071
 ; Patent No. 6107324

GENERAL INFORMATION:
 APPLICANT: Behan, Dominic
 APPLICANT: Chalmers, Derek
 TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
 TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arena Pharmaceuticals, Inc.
 STREET: 6166 Nancy Ridge Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/292,071
 FILING DATE: April 14, 1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Rosen
 REGISTRATION NUMBER: 39,822
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 564-6525
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein

US-09-292-071-25

Query Match 13.1%; Score 258; DB 3; Length 470;
 Best Local Similarity 24.7%; Pred. No. 1,4e-15;
 Matches 89; Conservative 63; Mismatches 155; Indels 54; Gaps 12;

15 LSPFLAFKLTSLGF-----IIGSVVGNLLISILYKDKTLHRAVYFLLDCCSDI 67

DB 61 LSPSSLLHDEKNSALLTAVIITLTAGNLTMAVSLKELONATYFLMSLAIDML 120
 QY 68 LSAICFPFVNSVKNSTWYGLTYKVIATFLVGLSCFHTAFMLFCISVTRYLAIA----- 124
 DB 121 LLGFLVMPVSMITLYGRMPLPSKLCVAVIYLDVLESTASIMHLCALSLDRVAIQNPIS 180
 QY 125 -HHREYTKRLTFWTCIAICMVWFLSVMAFP-PVLDVGYTSFIREDOCTQHSFRAN 182
 DB 181 HHSRNSRTRKAFUKITA-----WITISVIGSMIPVGLDODDSKVEKSGCLL-----AD 230
 QY 183 DSLGEMLLALILATOLVYLKIFVHBRKMKP---VOPVAVSONMTFHGASGQAANL 242
 DB 231 DN--FVLIGSFVSFPIITLIMVITYFL-----TKSLQKATLC-----VSDIGTRA 275
 QY 243 WLAGRCRPTPTLIGI-----RONANTGRRRLVLDEFKMEKRISRMFYMTFL 293
 DB 276 KLASRF--LQSSLSSEKLFORSIHREPGSTYGR---TMSISNEQACAVLGIVFPL 330
 QY 294 FLTMGPYLVACYWVFAR---GPVPPGFLTAAVWMSFAOGINPFVCIFSNRELRCP 350
 DB 331 FVMMCPFITINMAVICKESCNEVIGALLNVFWIGILSSAVNPVYTLTKITRRASNF 390
 QY 351 S 351
 DB 391 S 391

RESULT 5

US-09-292-069A-25
 ; Sequence 25, Application US/09292069A
 ; Patent No. 6140509

GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Foster, Richard J.
 APPLICANT: Glen, Robert C.
 APPLICANT: Lawless, Michael S.
 APPLICANT: Law, Chen W.
 APPLICANT: Liu, Qian
 APPLICANT: Russo, Joseph F.
 APPLICANT: Smith, Julian R.
 APPLICANT: Thomsen, William J.
 TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
 TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators
 TITLE OF INVENTION: Thereof
 FILE REFERENCE: AREN0033
 CURRENT APPLICATION NUMBER: US/09/292,069A
 CURRENT FILING DATE: 1999-04-14
 PRIOR APPLICATION NUMBER: 60/090,783
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/112,909
 PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 60/123,000
 PRIOR FILING DATE: 1999-03-05
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 25
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: NO. 6140509e1
 OTHER INFORMATION: Sequence

US-09-292-069A-25

Query Match 13.1%; Score 258; DB 4; Length 470;
 Best Local Similarity 24.7%; Pred. No. 1,4e-15;
 Matches 89; Conservative 63; Mismatches 155; Indels 54; Gaps 12;

15 LSPFLAFKLTSLGF-----IIGSVVGNLLISILYKDKTLHRAVYFLLDCCSDI 67

Db 61 LSPGSLHJQKNSALLTAVIILLIAGNILLVAVSLERKLOANTNFMLSLAD 120
Qy 68 LRSALCFPEVNSVKNKSGTWGTGLTCKYIAFGVYSCHETAMLCISTRLAIA--- 124
Db 121 LAGFVMPVSMILLIYGYWMPLEPSKLCAYWYLDVLESTASIMHLCAISLDRAVAIONPI 180
Qy 125 -HHREYTRKLFMTGLAVICWMTLSVMAAF-PVLDVGTYSFIREDOCTFQHSFRAN 182
Db 181 HHSRNSRKAFKLTIA---WVTISVGISMPLVPGLODDSVREKSCLL-----AD 230
Qy 183 DSLGFMILLALILLATOLVYLKLFVHRRKKMPVOFAAVSQNTFHPGASGOAAN 242
Db 231 DN-EVLIGSFVSPFLITIMTYTEL-----TKSLQKATLC-----VSDGTRA 275
Qy 243 WLAGRGFTPTLTGT-----RQANNTGRRRLVLDFEKKERISMFTYMTFL 293
Db 276 KLASFSF-LPOSSLSSEKLFORSIRHEPGSYGRR--TMOISNEOKACKVLGIYFFL 330
Qy 294 FTLLGPIYVACYWYFAR---GPVYPGFLTAAVMMSFAQAGINPVCIFSRRLRCF 350
Db 331 FVVMCPPEFTIMAVTCKESCNEVDIGALLNVWIGVSSAVNPLVYTLFENKTYRSAP 390
Qy 351 S 351
Db 391 S 391

RESULT 6
US-08-570-157-7
Sequence 7, Application US/08570157
Patent No. 5750353

GENERAL INFORMATION:
APPLICANT: Koplin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P. C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,157
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/109001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-570-157-7

Query Match 13.1%; Score 257.5; DB 1; Length 453;
Best Local Similarity 24.1%; Pred. No. 1,4e-15;

Matches 91; Conservative 63; Mismatches 170; Indels 53; Gaps 9;
Qy 16 SPLTAFLKLSLGIITISVAVGNLLISILYKOKTIRAPRYFLDCCSILSALCFP 75
Db 64 SDNLWARIWYSVIFLVSFGLNLLIIVNMRRLRTTNSFLLSLASDLMAVAVLCMP 123
Qy 76 FVF-NSVKNKSGTWGTGLTCKYIAFGVYSCHETAMLCISTRYLAIAHHREYTRK 133
Db 124 FTLLPIMEN---FIREVICRAAAYFMGLSVSTRLVAISTERSAICNPLKSRWQ 180
Qy 134 TFWTGLAVICWMTLSVMAAFPPVLDVGYTSFIRE---DOCTFOHNSFRANDSLGFM 189
Db 181 TRSAAYVIAATWVLSLIMIPLYVKNKTYTFPKMDRVRGHCRLWMSKVQQA-WVVL 239
Qy 190 LLAIIILATOLVYLKLFVHRRKKMPVOFAAVSQNTFHPGASGOAANLAGGR 249
Db 240 LTLTFLFIPGVYMI-VAAGLISRELYGIOPEMDLNKAKAHKNGVS----- 285
Qy 250 GPPPEPL-----LGIRONANTGRRRLVLDFEKKME-----KRISR 285
Db 286 -FTTIPSGDEGDCYIOYTKRRNTMEMSTLTPSVCTKMDPARINNSEAKLAKKRYIR 343
Qy 286 MFTYMTFLTLMGPVYVACYWYF---ARGVYPGFLTAAVMMSFAQAGINPVCIFS 342
Db 344 MLIVIAMFICWMPFIVANWKAFLDELASNTLGAIPISLHLSYSTACVNPILIYCFM 403
Qy 343 NRELRCFSTTLTYCRK 359
Db 404 NKRRKKAFLGTFFSSCIR 420

RESULT 7
US-09-292-071-33
Sequence 33, Application US/09292071
Patent No. 6107324

GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Th
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arena Pharmaceuticals, Inc.
STREET: 6166 Nancy Ridge Drive
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,071
FILING DATE: April 14, 1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Rosen
REGISTRATION NUMBER: 39,822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 564-6525
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-292-071-33

Query Match 13.1%; Score 256.5; DB 3; Length 478;
 Best Local Similarity 23.9%; Pred. No. 1.9e-15;
 Matches 83; Conservative 64; Mismatches 150; Indels 51; Gaps 11;

QY 30 IIVSVVGNLLISILVKKDTLHRAPIYFLIDCCSDILSAICFPFVNSVKNSTWY 89
 DB 84 VILITAGNIIIVMAVSEKRIKQNTNIFLMSIADMLGLVMPVSMITLIGYRML 143
 QY 90 GLTTCVIAFLVGLSCFHTAFMFCISVTRYLAIA-----HHREYTKLTFWTCLAVICW 145
 DB 144 PSKLCAMVIYLDVLPSTASIMHLCASIDRYVAIQNPINHRSNRSNTRAFKIIA-----V 199
 QY 146 WTLVSAAMP-PVLDVGYTSFIREDQCTFOHRSFRANDS-IGFMILLALILATOL-VY 202
 DB 200 WTIISVIGSMPIVFGLODDSKVFKESGLLADNDFVLIGSVSFFPLTIMVITYCLTIT 259
 QY 203 L---KLIFVHDKRKKMP---VOFVAASONTFHPGASQAANWLAGFGGPTPTL 256
 DB 260 VLRROALMLHGHTEEPGLSLDLFKCKRN-----TAEENSAN----- 299
 QY 257 LGIRONANTGRRRL-----VLDEFKMERISRMFYIMFLFLTMGPYLVACYWY 309
 DB 300 ---PNODNARRRRKKRRPRGTMQAINNERAKKAVIGIVFVFLIMCFFPITINIAV 355

QY 310 FAR---GPVVGGLTAAVWMSFAQAGINPFVCIFSNRELRCFSTTL 354
 DB 356 ICKESCNEVDIGALLNVFWIGILSSAVNPVLTLEFKITRRASFNTL 403

RESULT 8
 US-09-292-069A-33
 : Sequence 33, Application US/09292069A
 : Patent No. 6140509
 : GENERAL INFORMATION:
 : APPLICANT: Behan, Dominic P
 : APPLICANT: Chalmers, Derek T
 : APPLICANT: Foster, Richard J
 : APPLICANT: Glen, Robert C
 : APPLICANT: Lawless, Michael S
 : APPLICANT: Liaw, Chen W
 : APPLICANT: Liu, Qian
 : APPLICANT: Russo, Joseph F
 : APPLICANT: Smith, Julian R
 : APPLICANT: Thomson, William J
 : TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
 : TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators
 : FILE REFERENCE: AREN0033
 : CURRENT APPLICATION NUMBER: US/09/292,069A
 : CURRENT FILING DATE: 1999-04-14
 : PRIOR APPLICATION NUMBER: 60/090,783
 : PRIOR FILING DATE: 1998-06-26
 : PRIOR APPLICATION NUMBER: 60/112,909
 : PRIOR FILING DATE: 1998-12-18
 : PRIOR APPLICATION NUMBER: 60/123,000
 : PRIOR FILING DATE: 1999-03-05
 : NUMBER OF SEQ ID NOS: 33
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 33
 : LENGTH: 478
 : TYPE: PRT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of Artificial Sequence: No. 6140509e1
 : US-09-292-069A-33

Query Match 13.1%; Score 256.5; DB 4; Length 478;
 Best Local Similarity 23.9%; Pred. No. 1.9e-15;
 Matches 83; Conservative 64; Mismatches 150; Indels 51; Gaps 11;

QY 30 IICVSVGNLLISILVKKDTLHRAPIYFLIDCCSDILSAICFPFVNSVKNSTWY 89

DB 84 VILITAGNIIIVMAVSEKRIKQNTNIFLMSIADMLGLVMPVSMITLIGYRML 143
 QY 90 GLTTCVIAFLVGLSCFHTAFMFCISVTRYLAIA-----HHREYTKLTFWTCLAVICW 145
 DB 144 PSKLCAMVIYLDVLPSTASIMHLCASIDRYVAIQNPINHRSNRSNTRAFKIIA-----V 199
 QY 146 WTLVSAAMP-PVLDVGYTSFIREDQCTFOHRSFRANDS-IGFMILLALILATOL-VY 202
 DB 200 WTIISVIGSMPIVFGLODDSKVFKESGLLADNDFVLIGSVSFFPLTIMVITYCLTIT 259
 QY 203 L---KLIFVHDKRKKMP---VOFVAASONTFHPGASQAANWLAGFGGPTPTL 256
 DB 260 VLRROALMLHGHTEEPGLSLDLFKCKRN-----TAEENSAN----- 299
 QY 257 LGIRONANTGRRRL-----VLDEFKMERISRMFYIMFLFLTMGPYLVACYWY 309
 DB 300 ---PNODNARRRRKKRRPRGTMQAINNERAKKAVIGIVFVFLIMCFFPITINIAV 355

QY 310 FAR---GPVVGGLTAAVWMSFAQAGINPFVCIFSNRELRCFSTTL 354
 DB 356 ICKESCNEVDIGALLNVFWIGILSSAVNPVLTLEFKITRRASFNTL 403

RESULT 9
 US-08-118-270-19
 : Sequence 19, Application US/08118270
 : Patent No. 5508384
 : GENERAL INFORMATION:
 : APPLICANT: Murphy, Randall B.
 : APPLICANT: Schuster, David I.
 : TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 : TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 : NUMBER OF SEQUENCES: 348
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEIMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/118,270
 : FILING DATE: 09-SEP-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/943,236
 : FILING DATE: 10-SEP-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Townsend, Kevin G.
 : REGISTRATION NUMBER: 34,033
 : REFERENCE/DOCKET NUMBER: MURPHY-2A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-628-5197
 : TELEFAX: 202-737-3528
 : TELEX: 248633
 : INFORMATION FOR SEQ ID NO: 19:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 330 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : US-08-118-270-19

Query Match 13.0%; Score 255; DB 1; Length 330;
 Best Local Similarity 25.3%; Pred. No. 1.7e-15;
 Matches 89; Conservative 60; Mismatches 153; Indels 50; Gaps 13;

QY 27 LGFTIGSVGNLLISLLVNDKTLHRAVYFLDLCCSDILRSACIFEPVNSVKNK-S 85
DB 8 VGFLLVTVGNLVIAVLTSLRALRAPQNLFLVSIASADILVATLMPF---SLANEIM 64
QY 86 TWYGTGTCVKVIAFLVLSGCFHTAFMLFCISVTRYLAIHHRFYTKRLFTWTCIAVICW 145
DB 65 YWYFGQWCGVYLAIDVLFCTSSIVHLCATSDRYSVQAVEYNLKRTPRRKATIVAV 124
QY 146 WLSVMAAPFPVLDVGTYSFIRED---OCTFOHRS-FRANSLGEMILLALILILATO 199
DB 125 WLISAVISPEPLV-----SLYROPDGAAPQCGINDETWYILSSCIGSFAPCLITL--- 176
QY 200 LVYLKLIFFVHDR-----KMKPVQFVAVSONMTFHGPGASGQAANWL---AGFGRG 250
DB 177 LVYAR-IYRAKRRRTLTSEKRAV-----GPDGASPTTENGIGAAAGART 222
QY 251 PTPPTLLGIRQANNTGRRRLVLDERKMKRISRMFYIMTFLELTMGP-YLVACYWRY 309
DB 223 GTRFSLRRRRRASSVCRRK-----AQAEREKTFVLALVFLCWPFFFIYSLXGI 275
QY 310 FARGPVVPGGFLTAAVWMSFAQAGINPFCIFSRELRCFSTLLYCRSR 361
DB 276 CREACQVPGPLFKEFFWIGYCNSLNPVITYVENQDFRPSFK-HILFRRRR 326

RESULT 10
PCT-US93-08528-19

Sequence 19, Application PC/TUS9308528

GENERAL INFORMATION:

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MORPHY-2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 246633

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 330 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US93-08528-19

Query Match 13 0%; Score 255; DB 5; Length 330;

Best Local Similarity 25.3%; Pred. No. 1,7e-15;

Matches 89; Conservative 60; Mismatches 153; Indels 50; Gaps 13;

QY 27 LGFTIGSVGNLLISLLVNDKTLHRAVYFLDLCCSDILRSACIFEPVNSVKNK-S 85
DB 8 VGFLLVTVGNLVIAVLTSLRALRAPQNLFLVSIASADILVATLMPF---SLANEIM 64
QY 86 TWYGTGTCVKVIAFLVLSGCFHTAFMLFCISVTRYLAIHHRFYTKRLFTWTCIAVICW 145
DB 65 YWYFGQWCGVYLAIDVLFCTSSIVHLCATSDRYSVQAVEYNLKRTPRRKATIVAV 124
QY 146 WLSVMAAPFPVLDVGTYSFIRED---OCTFOHRS-FRANSLGEMILLALILILATO 199
DB 125 WLISAVISPEPLV-----SLYROPDGAAPQCGINDETWYILSSCIGSFAPCLITL--- 176
QY 200 LVYLKLIFFVHDR-----KMKPVQFVAVSONMTFHGPGASGQAANWL---AGFGRG 250
DB 177 LVYAR-IYRAKRRRTLTSEKRAV-----GPDGASPTTENGIGAAAGART 222
QY 251 PTPPTLLGIRQANNTGRRRLVLDERKMKRISRMFYIMTFLELTMGP-YLVACYWRY 309
DB 223 GTRFSLRRRRRASSVCRRK-----AQAEREKTFVLALVFLCWPFFFIYSLXGI 275
QY 310 FARGPVVPGGFLTAAVWMSFAQAGINPFCIFSRELRCFSTLLYCRSR 361
DB 276 CREACQVPGPLFKEFFWIGYCNSLNPVITYVENQDFRPSFK-HILFRRRR 326

RESULT 11

US-07-817-920-8

Sequence 8, Application US/07817920

Patent No. 5360735

GENERAL INFORMATION:

APPLICANT: Weinshank, Richard L

APPLICANT: Branciek, Theresa

TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/817,920

FILING DATE: 19920108

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 1795/39318

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-977-9550

TELEFAX: 212-664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 471 amino acids

TYPE: AMINO ACID

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

IMMEDIATE SOURCE:

CLONE: 5-HT2

US-07-817-920-8

| | | | | |
|--------------------------|--------|--------------------|------------|-------------|
| Query Match | 12.98; | Score 253.5; | DB 1; | Length 471; |
| Best Local Similarity | 24.88; | Pred. No. 3.4e-15; | | |
| Matches 84; Conservative | 61; | Mismatches 147; | Indels 47; | Gaps 11 |

```

Oy 30 IIGSVGNLLISLWKDTLHAPYFLLDCCSDILRSALIOFPFVNSVKNSTMY 89
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 84 VILITIGNILIVMVASLEKKLQNAWYIFLMSLADMLGELVPMVSMULTLYGRMPL 143
Oy 90 GILTCYIAELGVLSCPEHTAFMLFCISVTRYLAIA---HHRFYKRLTEWTCIAICWV 145
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 144 PSKCANWYIYLDVLEFSAASIMHLCAISLDRVYAQNPIHHSRFRSKRAFLKIIA----V 199
Oy 146 WTLISVANAAP-RVLDVGTYSFIREDOCTFOHRSFRANDSIGFMLALILATOLUYLK 204
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 200 WTLISVGISMPRPVFGGLDDSGKVFREGSGLL-----ADDN--FVLISFVSFFILTIMV 255
Oy 205 LIEFVHDBRRKKKRPQVFAVANSQNWTEHGPGASGQAAANLAGEGRGPPPLTIGI---- 255
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 IITYEL-----TIKSLQKBAIICL-----VSDLGTRAKLASFSF--LPQSLISEKILFQ 296
Oy 260 -----RQANANTGRRRLVLDEFFKMEKRISRFYIMTELEFLTLMPRYLYACTWRFRAR--- 312
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 RSHIREGSGTYGR--TMOISINSBOKACKYLGIVPEFLFVVMQCPFITINIMAYICKESC 353
Oy 313 GPVVGGEFLTAAMVMSFAQINGFVCIQISNRRLRQCS 351
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 354 NEDVIGALLNVFWIGYLISSAVNPLVYTLLEKTKYRSASF 392

```

RESULT 12
US-08-370-542-7

; Sequence 7, Application US/08370542
; Patent No. 5476782

GENERAL INFORMATION:
APPLICANT: Weinschank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1E RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

```

? SEQUENCE CHARACTERISTICS:
? LENGTH: 471 amino acids
? type: amino acid
? STRANDEDNESS: unknown
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? HYPOTHEITICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
US-08-370-542-7

```

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 12.9%; | Score 253.5; | DB 1; | Length 471; |
| Best Local Similarity | 24.8%; | Pred. NO. 3.4e-15; | | |
| Matches 84; | Conservative 61; | Mismatches 147; | Indels 47; | Gaps 11; |

```

QY 30 IIGSVGNLLISLWKDKRIHAPYFLDLCCSOLISALICEFPFVNSYKNGSTWY 89
Db 84 VIITIGNITLIVMAVSELEKKLQNTATNYFTLMSLAIDMLGLFVMPVSMITLIXGYMPL 143
QY 90 GTLLCKYIAFLGVLSCEPHTAFMLFCISVTRILAA----HHREYTKRLFEWTCIAYICWY 145
Db 144 PSKICAWIYIADVLFTASIMHLCAISLDYRVAIQNHHSRFRNSRKALKIITA-----V 199
QY 146 WTLSVAAAF-P-VILDVGTYSEFIREDOCTOHRSFRAHDSLGFMILLALILATOLVYLK 204
Db 200 WTISVIGSMIPRPGVLQDDSKVFRGSGCL-----ADGN--FLVISFVSFPLPLTW 251
QY 205 LIEFVHRRKKKKPQVFAAANSQNTWTFPGSGAGGAAANLAGGRCPTPTLLGI----- 259
Db 252 ITYEL-----TIKSLQKEATLC-----VSDIGTRAKLASESF--LPQSSISEKLFQ 296
QY 260 -----RQANNTGRRRLVLDEPFMEKRISRMFYIMTFLFLTNGPRYLVAQYMWYFAR--- 312
Db 297 RSIHREGSYTGR---TWQISINEQACAVGLGIVEFLFYVMCOPFITINIMAYICKESC 353
QY 313 GPVVPGGFLTAAMNSFAQAGINPFCVIFISNRELRCFS 351
Db 354 NEDVIGALLNFWNIGTSSVNPDLVTTLENKTKYTSAFS 392

```

RESULT 13

US-08-117-006-8
; Sequence 8, Application US/08117006

? Patent No. 5639652
 ? GENERAL INFORMATION:
 ? APPLICANT: Weinsbank, Richard L.
 ? APPLICANT: Branchek, Theresa
 ? APPLICANT: Hartig, Paul R.
 ? TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND
 ? TITLE OF INVENTION: USES THEREOF
 ? NUMBER OF SEQUENCES: 9
 ? CORRESPONDENCE ADDRESS:

TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
CLONE: 5-HT2
US-08-117-006-8

Query Match 12.9%; Score 253.5; DB 1; Length 471;
Best Local Similarity 24.8%; Pred. No. 3.4e-15;
Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

OY 30 IIGSVVGNLLISLLKKKTLHRAPIYFLDCCSDILRSALCPFFVNSVNGSTWTY 89
DB 84 VILITAGNILLVMAVSLERKLNATNFTLSLADMLGLFVMPVSMILTYGYRPL 143
OY 90 GLTCKVIAFLGLVSCFHTAFMLFCISVTRYLAIA---HHRYTKRLTFWTCLAVICW 145
DB 144 PSKLCAMVYLDVLFSTASIMHLCALSLDRYVAIONPIHHSRNSRKAKLKITA---V 199
OY 146 WTLVSAMAF-PVLVDGYTSFIREDOCTFOHRSFRANDSLGFMILLALITLALQVLYLK 204
DB 200 WTLISGISMPIPVFGLDDSKVFEKSGCLL-----ADDN--FVLISFVSFFIPLTIMV 251
OY 205 LIFFVDRKKMPVQFAVAVSONMTFHGPGASGQAANWLAGFGRPPTPLIGI----- 259
DB 252 ITYFL---TISLQKENTLC-----VSDLGTRAKLASFS--LPQSSLSSEKLFQ 296
OY 260 ---RQANNTGRRLLVLDEFKMKRISRMFYIMTFLTLMGPLYVACYWRYFAR--- 312
DB 297 RSIHREPGSYTGR---TMQISINEQKACKVIGIVFLEFVVMCPFITINIMAVICKESC 353
OY 313 GPVVGGLTAAVWMSFPAQAGINPVCIFSNRELRCFS 351
DB 354 NEDVIGALLNVFWIGYLSAVNPVLYTLFNTKTYRSAFS 392

RESULT 14
US-08-216-594-8

Sequence 8, Application US/08216594

Patent No. 5652113

GENERAL INFORMATION:

APPLICANT: Weinshank, Richard L.

APPLICANT: Branchek, Theresa

APPLICANT: Hartig, Paul R.

TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/216,594

FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
CLONE: 5-HT2
US-08-216-594-8

Query Match 12.9%; Score 253.5; DB 1; Length 471;
Best Local Similarity 24.8%; Pred. No. 3.4e-15;
Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

OY 30 IIGSVVGNLLISLLKKKTLHRAPIYFLDCCSDILRSALCPFFVNSVNGSTWTY 89
DB 84 VILITAGNILLVMAVSLERKLNATNFTLSLADMLGLFVMPVSMILTYGYRPL 143
OY 90 GLTCKVIAFLGLVSCFHTAFMLFCISVTRYLAIA---HHRYTKRLTFWTCLAVICW 145
DB 144 PSKLCAMVYLDVLFSTASIMHLCALSLDRYVAIONPIHHSRNSRKAKLKITA---V 199
OY 146 WTLVSAMAF-PVLVDGYTSFIREDOCTFOHRSFRANDSLGFMILLALITLALQVLYLK 204
DB 200 WTLISGISMPIPVFGLDDSKVFEKSGCLL-----ADDN--FVLISFVSFFIPLTIMV 251
OY 205 LIFFVDRKKMPVQFAVAVSONMTFHGPGASGQAANWLAGFGRPPTPLIGI----- 259
DB 252 ITYFL---TISLQKENTLC-----VSDLGTRAKLASFS--LPQSSLSSEKLFQ 296
OY 260 ---RQANNTGRRLLVLDEFKMKRISRMFYIMTFLTLMGPLYVACYWRYFAR--- 312
DB 297 RSIHREPGSYTGR---TMQISINEQKACKVIGIVFLEFVVMCPFITINIMAVICKESC 353
OY 313 GPVVGGLTAAVWMSFPAQAGINPVCIFSNRELRCFS 351
DB 354 NEDVIGALLNVFWIGYLSAVNPVLYTLFNTKTYRSAFS 392

RESULT 15
US-08-542-358-7

Sequence 7, Application US/08542358

Patent No. 5786155

GENERAL INFORMATION:

APPLICANT: Weinshank, Richard L.

APPLICANT: Branchek, Theresa

APPLICANT: Hartig, Paul R.

TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1E RECEPTOR AND USES THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,358
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39317-22/JFW/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-542-358-7

Query Match 12.9%; Score 253.5; DB 1; Length 471;

Best Local Similarity 24.8%; Pred. No. 3,4e-15;
Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

OY 30 IIGVGVGGLLSILVKKTLHRAVYVLLDCCSDILRSALCPFVFNVSXNGSTWY 89
DB 84 VILLITAGNLTVMVSEKLLQNNATNYFLMSLAIDMLGLVMPVSMLTLYGRWPL 143
OY 90 GLTCKVIAFLGVLSCFHTAFMLFCISVRYLAIA---HHRFYTKLFETCLAVICWY 145
DB 144 PSKLCVWYLDVLFSTASIMLCALSDRYVALQNPFIHSRNSKTKALKIIA---V 199
OY 146 WLSYVMAFP-DVLDVGYTSFIREDDQCTFHRSFRANDSLGFMILLALILATOLVLYK 204
DB 200 WTISVIGSMPIVFGLODSKVEKESCLL-----ADDN--FVLIGSFVSFPLTIWY 251
OY 205 LIEFVHDRKKMPVQFVAVSONWTFHGGASGQAANMLAGRGKPTPTLLGT----- 259
DB 252 IITYFL---TISLQKEATLC-----VSDIGTRAKIASFSF--LPSSLSSEKLFQ 296
OY 260 ---RQNNNTGRRLVYDEFKMERKISRMFYIMTFLTLMGPLYLVACVWRVFPAR--- 312
DB 297 RSIHREPGSYTER--TWQSTSNQKACKVLGIVFELVVMWCPFTINIMAVICKESC 353
OY 313 GPVVGGEFLTAAVMMSFAQAGINPFVCIPSNBELRCFS 351
DB 354 NEDVIGALLNVEWIGYLSAVNPLVYTLFNKTYRSASF 392

Search completed: July 19, 2002, 14:39:37
Job time: 158 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: July 19, 2002, 14:38:44 ; Search time 110.32 Seconds

(without alignments)
1180.500 Million cell updates/sec

Title: US-09-698-419-14

Perfect score: 1963
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
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| 2 | 1963 | 100.0 | 370 | 16 | US-09-264-041-2 Sequence 2, Appl1 |
| 3 | 1963 | 100.0 | 370 | 17 | US-09-383-745-1 Sequence 1, Appl1 |
| 4 | 1963 | 100.0 | 370 | 18 | US-09-416-760-28 Sequence 28, Appl1 |
| 5 | 1963 | 100.0 | 370 | 18 | US-09-416-760A-28 Sequence 28, Appl1 |
| 6 | 1963 | 100.0 | 370 | 18 | US-09-417-044-26 Sequence 26, Appl1 |
| 7 | 1963 | 100.0 | 370 | 18 | US-09-427-653-2 Sequence 2, Appl1 |

| 8 | 1963 | 100.0 | 370 | 19 | US-09-544-254-2 | Sequence 2, Appl1 |
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| 9 | 1963 | 100.0 | 370 | 20 | US-09-622-439-4 | Sequence 4, Appl1 |
| 10 | 1963 | 100.0 | 370 | 20 | US-09-622-439-24 | Sequence 24, Appl1 |
| 11 | 1963 | 100.0 | 370 | 20 | US-09-698-419-14 | Sequence 14, Appl1 |
| 12 | 1963 | 100.0 | 370 | 22 | US-09-875-076-26 | Sequence 26, Appl1 |
| 13 | 1963 | 100.0 | 370 | 22 | US-09-876-252-28 | Sequence 28, Appl1 |
| 14 | 1963 | 100.0 | 370 | 23 | US-09-988-922-16 | Sequence 16, Appl1 |
| 15 | 1963 | 100.0 | 370 | 24 | US-10-043-943-2 | Sequence 2, Appl1 |
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| 36 | 1274.5 | 64.9 | 373 | 16 | US-09-760-354A-2 | Sequence 2, Appl1 |
| 37 | 1270.5 | 64.7 | 373 | 16 | US-09-200-302-1 | Sequence 1, Appl1 |
| 38 | 998.5 | 50.9 | 375 | 17 | US-09-321-636-2 | Sequence 2, Appl1 |
| 39 | 998.5 | 50.9 | 375 | 18 | US-09-416-760-18 | Sequence 18, Appl1 |
| 40 | 998.5 | 50.9 | 375 | 18 | US-09-416-760A-18 | Sequence 16, Appl1 |
| 41 | 998.5 | 50.9 | 375 | 18 | US-09-417-044-16 | Sequence 2, Appl1 |
| 42 | 998.5 | 50.9 | 375 | 20 | US-09-622-439-2 | Sequence 2, Appl1 |
| 43 | 998.5 | 50.9 | 375 | 20 | US-09-634-392-1 | Sequence 1, Appl1 |
| 44 | 998.5 | 50.9 | 375 | 22 | US-09-875-076-16 | Sequence 16, Appl1 |
| 45 | 998.5 | 50.9 | 375 | 22 | US-09-876-252-18 | Sequence 18, Appl1 |

ALIGNMENTS

RESULT 1
US-09-145-745-1
Sequence 1, Application US/09145745A
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14926 Receptor, A Novel G-Protein Coupled Receptor
FILE REFERENCE: 035800/169197
CURRENT APPLICATION NUMBER: US/09/145,745A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-145-745-1

Query Match 100.0%; Score 1963; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 4; 6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DCCSDILRAIKCPFFYFNSVKNSTWTYGLTCKVIAFLGVLSCHFTAFMLPISVTRY 120

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DB 301 YIVACYWRVFAAGPVVGGFLTAAVMMSFAQAGINPVCIFSNRELRCRCESTLLYCRKS 360
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DB 361 RLPREPYCVI 370
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RESULT 2

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US-09-264-041-2
Sequence 2, Application US/09264041
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Pathirana, Marie Sudam
APPLICANT: Kyaw, Hla
APPLICANT: Borowsky, Beth E.
TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF12 RECEPTOR
FILE REFERENCE: 58801
CURRENT APPLICATION NUMBER: US/09/264,041
CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0 - beta
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-264-041-2
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Query Match 100.0%; Score 1963; DB 16; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 361 RLPREPYCVI 370
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RESULT 3

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US-09-383-745-1
Sequence 1, Application US/09383745
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14926 Receptor, A Novel G-Protein Coupled Receptor
FILE REFERENCE: 035800/169197
CURRENT APPLICATION NUMBER: US/09/383,745
CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: 09/145,745
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-745-1
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Query Match 100.0%; Score 1963; DB 17; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 361 RLPREPYCVI 370
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RESULT 4

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US-09-416-760-28
Sequence 28, Application US/09416760
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Tsin
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled
FILE REFERENCE: AREN-0054
CURRENT APPLICATION NUMBER: US/09/416,760
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
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PRIOR APPLICATION NUMBER: 60/110,060
 PRIOR FILING DATE: 1998-11-27
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
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 PRIOR FILING DATE: 1999-02-26
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 PRIOR FILING DATE: 1998-11-20
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 PRIOR APPLICATION NUMBER: 60/137,127
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/137,131
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 PRIOR APPLICATION NUMBER: 60/156,634
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 PRIOR APPLICATION NUMBER: 60/156,653
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 PRIOR APPLICATION NUMBER: 60/157,281
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: 60/157,282
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: 60/156,633
 PRIOR FILING DATE: 1999-09-29
 NUMBER OF SEQ ID NOS: 146
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 28
 LENGTH: 370
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-416-760-28

Query Match 100.0%; Score 1963; DB 18; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4,6e-182;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 DLCCSDILRSATCPPEVENSVKNGSTWYGTLTCKVIAFLVLSCEHTAFMFCISVTR 120
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 DB 121 LAIAHREFTYKRLFTWCLAVICWMTLSVMAAPPVLDVGTYSFIREDDCTFOHRSFR 180
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 DB 181 ANDSLGFMILLALILLATQVLYLKIIFVHDKKKPVQVAAVSQNTFPGSGAQA 240
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 DB 301 YLVACYRVEFARGPVVGGFLLTAVMNSFAQAGINPEFCISNRLRCFSTLLYCKRS 360
 QY 361 RLPREPYCVI 370
 DB 361 RLPREPYCVI 370

RESULT 5
 US-09-416-760A-28
 Sequence 28, Application US/09416760A
 GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Lehmann-Brulstma, Karin
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Lowitz, Kevin P.
 APPLICANT: Lin, I-Lin
 APPLICANT: Dang, Huong T.
 APPLICANT: Chen, Ruoping
 APPLICANT: Liaw, Chen W.
 TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled
 FILE REFERENCE: AREN-0054
 CURRENT APPLICATION NUMBER: US/09/416,760A
 PRIOR FILING DATE: 1999-10-12
 PRIOR APPLICATION NUMBER: 09/170,496
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: 60/110,060
 PRIOR FILING DATE: 1998-11-27
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
 PRIOR APPLICATION NUMBER: 60/121,852
 PRIOR FILING DATE: 1999-02-26
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 PRIOR APPLICATION NUMBER: 60/123,944
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 PRIOR FILING DATE: 1999-03-12
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PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-416-760A-28

Query Match 100.0%; Score 1963; DB 18; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MANYSHADNIIQNLSPFLAFLKLSLGLIGSVVGNLLISILVYDKTLHRAPIYFLL 60
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DB 61 DLCCSDILRSALCFPEFVNSVKNKSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
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DB 241 ANMLAGFGRPPTPLTIGIRONANTTGRRLVLVDEFKMKRISRMFYIMTFELTLMGP 300
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DB 301 YIVACYWRFVANGPVVGGFELTAVMMSFAOAGINPVCIFSNRELRCFSTLLYCCKS 360
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DB 361 RLREPVCVI 370

RESULT 6
US-09-417-044-26
Sequence 26, Application US/09417044
GENERAL INFORMATION:
APPLICANT: Chen, Kuoping

APPLICANT: Dang, Huang T.
APPLICANT: Lin, T-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/417,044
CURRENT FILING DATE: 1999-10-12
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-417-044-26

Query Match 100.0%; Score 1963; DB 18; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANYSHADNIIQNLSPFLAFLKLSLGLIGSVVGNLLISILVYDKTLHRAPIYFLL 60
DB 1 MANYSHADNIIQNLSPFLAFLKLSLGLIGSVVGNLLISILVYDKTLHRAPIYFLL 60
QY 61 DLCCSDILRSALCFPEFVNSVKNKSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB 61 DLCCSDILRSALCFPEFVNSVKNKSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
QY 121 LAIAHHRFTYKRLTFWCLAVICWMTLSVMAFPVLDVGTSTFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWCLAVICWMTLSVMAFPVLDVGTSTFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALITATOLVYKLIFFVHRRKMKPVQFAVAVSONMTPHFGASGOAA 240
DB 181 ANDSLGFMILLALITATOLVYKLIFFVHRRKMKPVQFAVAVSONMTPHFGASGOAA 240
QY 241 ANMLAGFGRPPTPLTIGIRONANTTGRRLVLVDEFKMKRISRMFYIMTFELTLMGP 300
DB 241 ANMLAGFGRPPTPLTIGIRONANTTGRRLVLVDEFKMKRISRMFYIMTFELTLMGP 300
QY 301 YIVACYWRFVANGPVVGGFELTAVMMSFAOAGINPVCIFSNRELRCFSTLLYCCKS 360
DB 301 YIVACYWRFVANGPVVGGFELTAVMMSFAOAGINPVCIFSNRELRCFSTLLYCCKS 360
QY 361 RLREPVCVI 370
DB 361 RLREPVCVI 370

RESULT 7
US-09-427-653-2
Sequence 2, Application US/09427653A
GENERAL INFORMATION:
APPLICANT: Vogell, Gabriel
APPLICANT: Wood, Linda
TITLE OF INVENTION: G Protein-coupled Receptor CON202, Expressed in Brain
FILE REFERENCE: 28341/6264
CURRENT APPLICATION NUMBER: US/09/427,653A
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-427-653-2

Query Match 100.0%; Score 1963; DB 18; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVGNLLISILVYKDKTLHRAPIYELL 60
DB 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVGNLLISILVYKDKTLHRAPIYELL 60
QY 61 DLCCSDILRSALICFPFVENSVKNGSTWYGTGTLCKVIAFLGVLSCEFTAFMLFCISVTRY 120
DB 61 DLCCSDILRSALICFPFVENSVKNGSTWYGTGTLCKVIAFLGVLSCEFTAFMLFCISVTRY 120
QY 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVAAAFPPVLVDGTSFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVAAAFPPVLVDGTSFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALILATQVLYKLIFVHDKRKMKPVOFAAASQNTFHHGASGQAA 240
DB 181 ANDSLGFMILLALILATQVLYKLIFVHDKRKMKPVOFAAASQNTFHHGASGQAA 240
QY 241 ANMLAGFGRPPTPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFELTLMGP 300
DB 241 ANMLAGFGRPPTPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFELTLMGP 300
QY 301 YLVACYWRVFARGPVVGGLTAAVWMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
DB 301 YLVACYWRVFARGPVVGGLTAAVWMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
QY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370
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RESULT 8

US-09-544-254-2

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; Sequence 2, Application US/09544254
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: ELSHOUBAGY, NABIL
; APPLICANT: BERGSMA, DERK J.
; TITLE OF INVENTION: A G-PROTEIN COUPLED 7TM RECEPTOR
; FILE REFERENCE: GP-70432-D1
; CURRENT APPLICATION NUMBER: US/09/544,254
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/082,981
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/089,639
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/251,373
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-544-254-2
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Query Match 100.0%; Score 1963; DB 19; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVGNLLISILVYKDKTLHRAPIYELL 60
DB 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVGNLLISILVYKDKTLHRAPIYELL 60
QY 61 DLCCSDILRSALICFPFVENSVKNGSTWYGTGTLCKVIAFLGVLSCEFTAFMLFCISVTRY 120
DB 61 DLCCSDILRSALICFPFVENSVKNGSTWYGTGTLCKVIAFLGVLSCEFTAFMLFCISVTRY 120
QY 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVAAAFPPVLVDGTSFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVAAAFPPVLVDGTSFIREDOCTFOHRSFR 180
```

```
QY 181 ANDSLGFMILLALILATQVLYKLIFVHDKRKMKPVOFAAASQNTFHHGASGQAA 240
DB 181 ANDSLGFMILLALILATQVLYKLIFVHDKRKMKPVOFAAASQNTFHHGASGQAA 240
QY 241 ANMLAGFGRPPTPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFELTLMGP 300
DB 241 ANMLAGFGRPPTPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFELTLMGP 300
QY 301 YLVACYWRVFARGPVVGGLTAAVWMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
DB 301 YLVACYWRVFARGPVVGGLTAAVWMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
QY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370
```

RESULT 9

US-09-622-439-4

```
; Sequence 4, Application US/09622439
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel G protein coupled receptor protein
; FILE REFERENCE: Y9905
; CURRENT APPLICATION NUMBER: US/09/622,439
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: JP P1998-060245
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP P1999-026774
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-622-439-4
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Query Match 100.0%; Score 1963; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVGNLLISILVYKDKTLHRAPIYELL 60
DB 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVGNLLISILVYKDKTLHRAPIYELL 60
QY 61 DLCCSDILRSALICFPFVENSVKNGSTWYGTGTLCKVIAFLGVLSCEFTAFMLFCISVTRY 120
DB 61 DLCCSDILRSALICFPFVENSVKNGSTWYGTGTLCKVIAFLGVLSCEFTAFMLFCISVTRY 120
QY 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVAAAFPPVLVDGTSFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVAAAFPPVLVDGTSFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALILATQVLYKLIFVHDKRKMKPVOFAAASQNTFHHGASGQAA 240
DB 181 ANDSLGFMILLALILATQVLYKLIFVHDKRKMKPVOFAAASQNTFHHGASGQAA 240
QY 241 ANMLAGFGRPPTPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFELTLMGP 300
DB 241 ANMLAGFGRPPTPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFELTLMGP 300
QY 301 YLVACYWRVFARGPVVGGLTAAVWMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
DB 301 YLVACYWRVFARGPVVGGLTAAVWMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
QY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370
```

RESULT 10

US-09-622-439-24
; Sequence 24, Application US/09622439
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel G protein coupled receptor protein
; FILE REFERENCE: Y9905
; CURRENT APPLICATION NUMBER: US/09/622,439
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: JP P1998-060245
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP P1999-026774
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 24
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-622-439-24

Query Match 100.0%; Score 1963; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNTLSPLTAFLKLSLGFIIIGSVVGNLLISILVKKTLHRAPIYFLL 60
DB 1 MANYSHADNIIQNTLSPLTAFLKLSLGFIIIGSVVGNLLISILVKKTLHRAPIYFLL 60
QY 61 DICCSDLIRSAICFPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAFLFCISVTRY 120
DB 61 DICCSDLIRSAICFPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAFLFCISVTRY 120
QY 121 LAIAHREFTKRLTFMTCLAVICMWTLSVAAAFPPYLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHREFTKRLTFMTCLAVICMWTLSVAAAFPPYLDVGTYSFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAASQNMWTFHGPGASQAA 240
DB 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAASQNMWTFHGPGASQAA 240
QY 241 ANMLAGRGPTPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLWGP 300
DB 241 ANMLAGRGPTPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLWGP 300
QY 301 YLVACYRVARAGPVVPGGFLTAAVWMSFAOAGINPVCIFSNRELRCFSTTLTYCRKS 360
DB 301 YLVACYRVARAGPVVPGGFLTAAVWMSFAOAGINPVCIFSNRELRCFSTTLTYCRKS 360
QY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370

RESULT 11
US-09-698-419-14
; Sequence 14, Application US/09698419
; GENERAL INFORMATION:
; APPLICANT: Vogell, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
; FILE REFERENCE: 28341/6276NCP
; CURRENT APPLICATION NUMBER: US/09/698,419
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 09/481,794
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 09/454,399
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 09/429,517
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,555
; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: US 09/429,676
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,695
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/428,114
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/428,020
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/427,859
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/427,653
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-698-419-14

Query Match 100.0%; Score 1963; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNTLSPLTAFLKLSLGFIIIGSVVGNLLISILVKKTLHRAPIYFLL 60
DB 1 MANYSHADNIIQNTLSPLTAFLKLSLGFIIIGSVVGNLLISILVKKTLHRAPIYFLL 60
QY 61 DICCSDLIRSAICFPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAFLFCISVTRY 120
DB 61 DICCSDLIRSAICFPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAFLFCISVTRY 120
QY 121 LAIAHREFTKRLTFMTCLAVICMWTLSVAAAFPPYLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHREFTKRLTFMTCLAVICMWTLSVAAAFPPYLDVGTYSFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAASQNMWTFHGPGASQAA 240
DB 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAASQNMWTFHGPGASQAA 240
QY 241 ANMLAGRGPTPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLWGP 300
DB 241 ANMLAGRGPTPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLWGP 300
QY 301 YLVACYRVARAGPVVPGGFLTAAVWMSFAOAGINPVCIFSNRELRCFSTTLTYCRKS 360
DB 301 YLVACYRVARAGPVVPGGFLTAAVWMSFAOAGINPVCIFSNRELRCFSTTLTYCRKS 360
QY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370

RESULT 12
US-09-875-076-26
; Sequence 26, Application US/09875076
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-076-26

Query Match 100.0%; Score 1963; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANYSHADNIIQNSPLTAFLKLSLGIIVSVYGNLLISILVKKDTLRAPYFLL 60
DB 1 MANYSHADNIIQNSPLTAFLKLSLGIIVSVYGNLLISILVKKDTLRAPYFLL 60
QY 61 DLCCSDILRSALCFPEFVNSVKNSTWYGTCTCKVIAFLGVLSCHPTAFMELCISVTRY 120
DB 61 DLCCSDILRSALCFPEFVNSVKNSTWYGTCTCKVIAFLGVLSCHPTAFMELCISVTRY 120
QY 121 LAIAHREYTRKLTFTWCTAVICNWTLSVANAAPPVLDVGYSTFREDDQCFQHRSR 180
DB 121 LAIAHREYTRKLTFTWCTAVICNWTLSVANAAPPVLDVGYSTFREDDQCFQHRSR 180
QY 181 ANDSIGFMILLALLILLOLVYLKLIFFYHDKRKKKPVQVFAAVSONMTFHGSGAGQAA 240
DB 181 ANDSIGFMILLALLILLOLVYLKLIFFYHDKRKKKPVQVFAAVSONMTFHGSGAGQAA 240
QY 241 ANWLAGFGRGPTPTLLGIRONANTGRRRLVLDDEKKEKRISRMFYIMTFELTLMGP 300
DB 241 ANWLAGFGRGPTPTLLGIRONANTGRRRLVLDDEKKEKRISRMFYIMTFELTLMGP 300
QY 301 YLVACYWVFARGPVYVGGFLLTAAVMSFAQGINPEVCIFSNRELRLRCFSTLLYCRS 360
DB 301 YLVACYWVFARGPVYVGGFLLTAAVMSFAQGINPEVCIFSNRELRLRCFSTLLYCRS 360
QY 361 RLPRPYCVI 370

DB 361 RLPRPYCVI 370
RESULT 13
US-09-876-252-28
Sequence 28, Application US/09876252
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Lehmann-Brunisma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Lin
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled
FILE REFERENCE: AREN-0054
CURRENT APPLICATION NUMBER: US/09/876,252
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,951
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/152,524
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/151,114
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/108,029
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294

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PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH: 370
TYPE: PRF
ORGANISM: Homo sapiens
US-09-876-252-28

Query Match      100.0%; Score 1963; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANTSHADNLIQNLSPITAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
   |||||||
DB 1 MANTSHADNLIQNLSPITAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
   |||||||

QY 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
   |||||||
DB 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
   |||||||

QY 121 LAIAHHRFTKRLTFWTCLAVICMWTLISVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
   |||||||
DB 121 LAIAHHRFTKRLTFWTCLAVICMWTLISVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
   |||||||

QY 181 ANDSLGFMILLALILATOLVYLKLIFFVHDKRKKPVQFVAASQNTFHHGASGQAA 240
   |||||||
DB 181 ANDSLGFMILLALILATOLVYLKLIFFVHDKRKKPVQFVAASQNTFHHGASGQAA 240
   |||||||

QY 241 ANMLAGFGRGPPPTLLGIRONANTTGRRLVLDEFKMEKRSIRMEFYIMTFLETLTMGP 300
   |||||||
DB 241 ANMLAGFGRGPPPTLLGIRONANTTGRRLVLDEFKMEKRSIRMEFYIMTFLETLTMGP 300
   |||||||

QY 301 YIVACYWRFARGPVPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
   |||||||
DB 301 YIVACYWRFARGPVPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
   |||||||

QY 361 RLPREPYCVI 370
   |||||||
DB 361 RLPREPYCVI 370
   |||||||

RESULT 14
US-09-988-922-16
Sequence 16, Application US/09988922
GENERAL INFORMATION:
APPLICANT: Erding Hu
APPLICANT: Yuan Zhu
APPLICANT: Ganesh M. Sathe
APPLICANT: Joyce Yue Mao
APPLICANT: Wendy S. Halsey
APPLICANT: Jon Chambers
APPLICANT: Allison Isodel Muir
APPLICANT: Phillip Graham Szekeres
APPLICANT: Derek J. Bergsma
APPLICANT: Nabil A. Elshourbagy
APPLICANT: David Michalovich
APPLICANT: Pamela A. Lane
APPLICANT: Menelas N. Pangalos
APPLICANT: Melanie Robbins
APPLICANT: David Malcolm Duckworth
APPLICANT: Jeffrey Hill
APPLICANT: Ping Tsui
APPLICANT: Pankaj Agarwal
APPLICANT: Randall Forrest Smith
```

```

APPLICANT: Lisa Vawter
APPLICANT: Catherine E. Ellis
APPLICANT: Mahanandeeswar Gattu
APPLICANT: John W. Quillen, Jr.
APPLICANT: Erin M. Toland
APPLICANT: Steven Michael Foord
APPLICANT: Han Ngoc Trinh
APPLICANT: Alexander Taylor
APPLICANT: Henry Sarau
APPLICANT: Steven Ruben
APPLICANT: George H. Postle
APPLICANT: Michel Louis Souchet
APPLICANT: Philippe Laurent Robert
APPLICANT: Stephane Clement Krief
APPLICANT: Bernard Emile Joseph Gout
APPLICANT: Eve Mahe
TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES.
FILE REFERENCE: GP-70775B-C1
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 370
TYPE: PRF
ORGANISM: HOMO SAPIENS
US-09-988-922-16

Query Match      100.0%; Score 1963; DB 23; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANTSHADNLIQNLSPITAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
   |||||||
DB 1 MANTSHADNLIQNLSPITAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
   |||||||

QY 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
   |||||||
DB 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
   |||||||

QY 121 LAIAHHRFTKRLTFWTCLAVICMWTLISVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
   |||||||
DB 121 LAIAHHRFTKRLTFWTCLAVICMWTLISVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
   |||||||

QY 181 ANDSLGFMILLALILATOLVYLKLIFFVHDKRKKPVQFVAASQNTFHHGASGQAA 240
   |||||||
DB 181 ANDSLGFMILLALILATOLVYLKLIFFVHDKRKKPVQFVAASQNTFHHGASGQAA 240
   |||||||

QY 241 ANMLAGFGRGPPPTLLGIRONANTTGRRLVLDEFKMEKRSIRMEFYIMTFLETLTMGP 300
   |||||||
DB 241 ANMLAGFGRGPPPTLLGIRONANTTGRRLVLDEFKMEKRSIRMEFYIMTFLETLTMGP 300
   |||||||

QY 301 YIVACYWRFARGPVPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
   |||||||
DB 301 YIVACYWRFARGPVPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
   |||||||

QY 361 RLPREPYCVI 370
   |||||||
DB 361 RLPREPYCVI 370
   |||||||

RESULT 15
US-10-043-945-2
Sequence 2, Application US/10043945
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Pathirana, Marie Sudam
APPLICANT: Kyaw, Hla
APPLICANT: Borowsky, Beth E.
TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF12 RECEPTOR
FILE REFERENCE: 58801
```

: CURRENT APPLICATION NUMBER: US/10/043,945
 : CURRENT FILING DATE: 2002-01-10
 : PRIOR APPLICATION NUMBER: 09/264,041
 : PRIOR FILING DATE: 1998-03-08
 : NUMBER OF SEQ ID NOS: 2
 : SOFTWARE: PatentIn Ver. 2.0 - beta
 : SEQ ID NO 2
 : LENGTH: 370
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-10-043-945-2

Query Match 100.0% Score 1963; DB 24; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4.6e-182;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|-------------------------------------------------------------|-----|
| QY | 1 | MANYSHADNIIQNLSPITAFKLTSLGFLIGSVVGNLLISILVYKDKTLHRAPYYELL | 60 |
| Db | 1 | MANYSHADNIIQNLSPITAFKLTSLGFLIGSVVGNLLISILVYKDKTLHRAPYYELL | 60 |
| QY | 61 | DIICSDILRSALICPFVENSVMKNGSTWYGTLCVKYIAFLGVLSCFHTAFMFCISVTRY | 120 |
| Db | 61 | DIICSDILRSALICPFVENSVMKNGSTWYGTLCVKYIAFLGVLSCFHTAFMFCISVTRY | 120 |
| QY | 121 | LAIHHREYTKRLTFWTCIAVICMWTLSVMAFPVLDVGTYSFIREDOCTFOHRSFR | 180 |
| Db | 121 | LAIHHREYTKRLTFWTCIAVICMWTLSVMAFPVLDVGTYSFIREDOCTFOHRSFR | 180 |
| QY | 181 | ANDSIGFMILLALILATOLVYLKLIFFVHDKKMKPVQFAVAVSONWTFHGPASGOAA | 240 |
| Db | 181 | ANDSIGFMILLALILATOLVYLKLIFFVHDKKMKPVQFAVAVSONWTFHGPASGOAA | 240 |
| QY | 241 | ANMLAGFGRGPTPTLLGIRONANTTGRRLVLDLDEKMEKRISRMYINTFLFLTLWGP | 300 |
| Db | 241 | ANMLAGFGRGPTPTLLGIRONANTTGRRLVLDLDEKMEKRISRMYINTFLFLTLWGP | 300 |
| QY | 301 | YIVACYWRYEARGPVYPGGFLTAAYWMSFAQAGINPFVCLFSNRELRCESTTLVCRKS | 360 |
| Db | 301 | YIVACYWRYEARGPVYPGGFLTAAYWMSFAQAGINPFVCLFSNRELRCESTTLVCRKS | 360 |
| QY | 361 | RLPREYCVI 370 | |
| Db | 361 | RLPREYCVI 370 | |

Search completed: July 19, 2002, 14:42:30
 Job time: 226 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2002, 14:38:24 ; Search time 21.56 seconds

(without alignments)
2133.035 Million cell updates/sec

Title: US-09-698-419-14

Perfect score: 1963
Sequence: 1 MANSYSHADNLTQNLSPFLTA.....STLLYCKRNLPRPYCVI 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 378952 seqs, 124292526 residues

Total number of hits satisfying chosen parameters: 378952

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New: *
1: /cgn2_6/prodata/2/paa/BCT_NEW_COMB.pep: *
2: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep: *
4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep: *
5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep: *
6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep: *
7: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1963 | 100.0 | 370 | 6 | US-10-110-668-14 |
| 2 | 1963 | 100.0 | 370 | 6 | US-10-125-749-16 |
| 3 | 1963 | 100.0 | 370 | 6 | US-10-165-844-7 |
| 4 | 633 | 32.2 | 183 | 6 | US-10-103-313-389 |
| 5 | 577 | 29.4 | 144 | 6 | US-10-103-313-394 |
| 6 | 473 | 24.1 | 180 | 6 | US-10-103-313-379 |
| 7 | 470 | 23.9 | 143 | 6 | US-10-130-469-62 |
| 8 | 337.5 | 17.2 | 106 | 6 | US-10-130-469-30 |
| 9 | 264.5 | 13.5 | 478 | 6 | US-10-176-255-31 |
| 10 | 258 | 13.1 | 470 | 6 | US-10-176-255-25 |
| 11 | 257.5 | 13.1 | 453 | 6 | US-10-127-940-7 |
| 12 | 256.5 | 13.1 | 478 | 6 | US-10-176-255-33 |
| 13 | 253.5 | 12.9 | 470 | 6 | US-10-166-101-8 |
| 14 | 253 | 12.9 | 448 | 6 | US-10-127-940-3 |
| 15 | 252.5 | 12.9 | 470 | 7 | US-60-380-336-52 |
| 16 | 247.5 | 12.6 | 447 | 6 | US-10-157-031-10 |
| 17 | 243.5 | 12.4 | 388 | 6 | US-10-157-031-123 |
| 18 | 243.5 | 12.4 | 388 | 6 | US-10-157-031-124 |
| 19 | 241.5 | 12.3 | 460 | 6 | US-10-166-101-4 |
| 20 | 241 | 12.3 | 458 | 6 | US-10-176-255-27 |
| 21 | 239 | 12.2 | 422 | 6 | US-10-118-804-13 |
| 22 | 239 | 12.2 | 422 | 6 | US-10-166-101-3 |
| 23 | 237.5 | 12.1 | 451 | 6 | US-10-127-940-2 |
| 24 | 237.5 | 12.1 | 497 | 6 | US-09-568-255-2 |
| 25 | 237.5 | 12.1 | 497 | 6 | US-10-052-589-2 |
| 26 | 237.5 | 12.1 | 515 | 6 | US-10-130-461-11 |

| | | | | | | |
|----|-------|------|-----|---|--------------------|-------------------|
| 27 | 237 | 12.1 | 458 | 6 | US-10-176-255-29 | Sequence 29, App1 |
| 28 | 235.5 | 12.0 | 453 | 6 | US-10-127-940-4 | Sequence 4, App1 |
| 29 | 233.5 | 11.9 | 402 | 1 | PCT-US02-09785-750 | Sequence 750, App |
| 30 | 233.5 | 11.9 | 402 | 6 | US-10-165-844-10 | Sequence 10, App1 |
| 31 | 233.5 | 11.9 | 461 | 7 | US-60-389-987-371 | Sequence 371, App |
| 32 | 233.5 | 11.9 | 466 | 6 | US-09-952-680A-26 | Sequence 26, App1 |
| 33 | 233.5 | 11.9 | 466 | 6 | US-10-002-945-129 | Sequence 129, App |
| 34 | 232 | 11.8 | 565 | 6 | US-10-130-461-12 | Sequence 12, App1 |
| 35 | 230 | 11.7 | 428 | 6 | US-10-127-940-5 | Sequence 5, App1 |
| 36 | 229.5 | 11.7 | 501 | 7 | US-60-360-039-7013 | Sequence 7013, Ap |
| 37 | 228.5 | 11.6 | 443 | 6 | US-10-127-940-6 | Sequence 6, App1 |
| 38 | 227.5 | 11.6 | 466 | 6 | US-10-130-461-10 | Sequence 10, App1 |
| 39 | 227.5 | 11.6 | 466 | 6 | US-60-380-336-47 | Sequence 47, App1 |
| 40 | 227 | 11.6 | 365 | 6 | US-10-125-749-28 | Sequence 28, App1 |
| 41 | 227 | 11.6 | 445 | 6 | US-10-118-804-2 | Sequence 2, App1 |
| 42 | 226.5 | 11.5 | 346 | 4 | US-08-899-1128-30 | Sequence 30, App1 |
| 43 | 224 | 11.4 | 387 | 4 | US-08-899-1128-28 | Sequence 28, App1 |
| 44 | 224 | 11.4 | 387 | 7 | US-60-391-385-6 | Sequence 6, App1 |
| 45 | 222 | 11.3 | 443 | 6 | US-10-157-031-78 | Sequence 78, App1 |

ALIGNMENTS

```

RESULT 1
US-10-110-668-14
Sequence 14, Application US/10110668
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
TITLE OR INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
FILE REFERENCE: 28341/6276P
CURRENT APPLICATION NUMBER: US/10/110, 668
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 09/481,794
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: US 09/454,399
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US 09/429,517
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/429,555
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/429,695
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/427,859
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 09/427,653
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 14
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-10-110-668-14

Query Match 100.0%; Score 1963; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 3 4e-168;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 121 LAIAHRRYTKRLTWTCLAVICWVTLSSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
Db 121 LAIAHRRYTKRLTWTCLAVICWVTLSSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
OY 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
Db 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
OY 241 ANMLAGFGPGPTPTLLGIRONANTGRRRLVLDEFKMEKRISRMEYIMTFLETLMP 300
Db 241 ANMLAGFGPGPTPTLLGIRONANTGRRRLVLDEFKMEKRISRMEYIMTFLETLMP 300
OY 301 YLVACYWRVFARPGVPGGFLTAAYWMSFAQAGINPEVCIFSNRELRCFSTLLYCRKS 360
Db 301 YLVACYWRVFARPGVPGGFLTAAYWMSFAQAGINPEVCIFSNRELRCFSTLLYCRKS 360
OY 361 RLPREPYCVI 370
Db 361 RLPREPYCVI 370

RESULT 2
US-10-125-749-16
Sequence 16, Application US/10125749
GENERAL INFORMATION:
APPLICANT: Erding Hu
APPLICANT: Ganesh M. Sathe
APPLICANT: Joyce Yue Mao
APPLICANT: Wendy S. Halsey
APPLICANT: Jon Chambers
APPLICANT: Allison Isobel Muir
APPLICANT: Philip Graham Szekeres
APPLICANT: Usman Shabon
APPLICANT: Derek J. Bergsma
APPLICANT: Nabil A. Elshourbagy
APPLICANT: David Michalovich
APPLICANT: Pamela A. Lane
APPLICANT: Menelas N. Pangalos
APPLICANT: Melanie Robbins
APPLICANT: David Malcolm Duckworth
APPLICANT: Jeffrey Hill
APPLICANT: Ping Tsui
APPLICANT: Pankaj Agarwal
APPLICANT: Randall Forrest Smith
APPLICANT: Lisa Vawter
APPLICANT: Catherine E. Ellis
APPLICANT: Manhanandeeswar Gattu
APPLICANT: John W. Quillen, Jr.
APPLICANT: Erin M. Toland
APPLICANT: Steven Michael Foord
APPLICANT: Han Ngoc Trinh
APPLICANT: Alexander Taylor
APPLICANT: Henry Sarau
APPLICANT: Steven Ruben
APPLICANT: George H. Postle
APPLICANT: Michel Louis Souchet
APPLICANT: Philippe Laurent Robert
APPLICANT: Stephane Clement Krief
APPLICANT: Bernard Emile Joseph Gout
APPLICANT: Eve Mahe
TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: GP-707758-C1
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US/09/988, 922
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 370
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TYPE: PRT
ORGANISM: HOMO SAPIENS
US-10-125-749-16

Query Match 100.0%; Score 1963; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 3,4e-168;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MANYSHADNIIIONLSPLFAFLKTSIGFTIGSVGNLLISILLYVOKTLHRAPIYELL 60
Db 1 MANYSHADNIIIONLSPLFAFLKTSIGFTIGSVGNLLISILLYVOKTLHRAPIYELL 60
OY 61 DLCCSDILRSALCFPEVENSVKNGSTWYGTLLCKVIAFLGVLSCFHTAPMLFCISVTRY 120
Db 61 DLCCSDILRSALCFPEVENSVKNGSTWYGTLLCKVIAFLGVLSCFHTAPMLFCISVTRY 120
OY 121 LAIAHRRYTKRLTWTCLAVICWVTLSSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
Db 121 LAIAHRRYTKRLTWTCLAVICWVTLSSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
OY 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
Db 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
OY 241 ANMLAGFGPGPTPTLLGIRONANTGRRRLVLDEFKMEKRISRMEYIMTFLETLMP 300
Db 241 ANMLAGFGPGPTPTLLGIRONANTGRRRLVLDEFKMEKRISRMEYIMTFLETLMP 300
OY 301 YLVACYWRVFARPGVPGGFLTAAYWMSFAQAGINPEVCIFSNRELRCFSTLLYCRKS 360
Db 301 YLVACYWRVFARPGVPGGFLTAAYWMSFAQAGINPEVCIFSNRELRCFSTLLYCRKS 360
OY 361 RLPREPYCVI 370
Db 361 RLPREPYCVI 370

RESULT 3
US-10-165-844-7
Sequence 7, Application US/10165844
GENERAL INFORMATION:
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Hodge, Martin R.
APPLICANT: Hunter, John J.
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Welch, Nadine S.
TITLE OF INVENTION: Silos-Santiago, Immaculada
FILE REFERENCE: 35800/248302
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 09/088, 857
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 09/324, 465
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 09/464, 685
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: US 09/741, 783
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/145, 745
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: US 09/383, 745
PRIOR FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: US 09/234, 923
PRIOR FILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: US 09/340, 880
PRIOR FILING DATE: 1999-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 370
```

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-165-844-7

| | | | | |
|---------------------------|---------|---------------------|-------|-------------------|
| Query Match | 100.0%; | Score 1963; | DB 6; | Length 370; |
| Best Local Similarity | 100.0%; | Pred. No. 3,4e-168; | | |
| Matches 370; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |

| | | | | |
|----|-----|-----------------|--------------------------------------------------|-----|
| QY | 1 | MANTSHAADNLOU | SPLTAFLKLTSGFIIGSVGNLLISILYDKLHRAAPYFLL | 60 |
| | | | | |
| Db | 1 | MANTSHAADNLOU | SPLTAFLKLTSGFIIGSVGNLLISILYDKLHRAAPYFLL | 60 |
| | | | | |
| QY | 61 | DLCCSDILRSAICP | PEFVNSVKNGSMTYGTLCCKVIAFGLVSCFTTAMLCISVTRY | 120 |
| | | | | |
| Db | 61 | DLCCSDILRSAICP | PEFVNSVKNGSMTYGTLCCKVIAFGLVSCFTTAMLCISVTRY | 120 |
| | | | | |
| QY | 121 | LAIAMHFFYTKRLTF | WTICWWTLSVAAAFPPVLVDGTSFSFIEEDQCTFFOHRSEF | 180 |
| | | | | |
| Db | 121 | LAIAMHFFYTKRLTF | WTICWWTLSVAAAFPPVLVDGTSFSFIEEDQCTFFOHRSEF | 180 |
| | | | | |
| QY | 181 | ANDSLGFMLLATL | LITLTLTYLKLIFEVHDDRMRKRVQCEVAASQWTFHGGASGGQAA | 240 |
| | | | | |
| Db | 181 | ANDSLGFMLLATL | LITLTLTYLKLIFEVHDDRMRKRVQCEVAASQWTFHGGASGGQAA | 240 |
| | | | | |
| QY | 241 | ANMLAGRGCGTPT | TLGLIGIRONANTTGRRRLLVYDEKMKKRISRMEYIMTFEFLTMGP | 300 |
| | | | | |
| Db | 241 | ANMLAGRGCGTPT | TLGLIGIRONANTTGRRRLLVYDEKMKKRISRMEYIMTFEFLTMGP | 300 |
| | | | | |
| QY | 301 | YLVAQYWRVPA | RGVGVGGEFLTAAVMNSFAQAGINPEVCIFSNRELARCSTTLLYCRKS | 360 |
| | | | | |
| Db | 301 | YLVAQYWRVPA | RGVGVGGEFLTAAVMNSFAQAGINPEVCIFSNRELARCSTTLLYCRKS | 360 |
| | | | | |
| QY | 361 | RLPREPYCVI | 370 | |
| | | | | |
| Db | 361 | RLPREPYCVI | 370 | |
| | | | | |

```

RESULT      4
US-10-103-389
: Sequence 389: Application US/10103313
:
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P1207C1
: CURRENT APPLICATION NUMBER: US/10/103,313
: CURRENT FILING DATE: 2002-03-12
: NUMBER OF SEQ ID NOS: 653
:   Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 389
: LENGTH: 183
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (170)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: US-10-103-313-389

```

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 32.2% | Score 633; | DB 6; | Length 183; |
| Best Local Similarity | 62.9% | Pred. NO. 2.9e-49; | | |
| Matches 112; Conservative | 31; | Mismatches 33; | Indels 2; | Gaps 1; |

[illegible]

QY 119 RYLALAHHRFYKRLTEWTCCLAVICWWTLSVMAAFPPVLVDGYSFIREEDCTFOH 176
|:|||||. |: | | | | | | | | | | | | | | | | | | | | | |
Db 126 RYMALAHHRFYAKRMTLWTCALVICAWTLSVMAAFPVPDVGTXKFIREDCI FEH 183

```

RESULT 5
US-10-103-313-394
: Sequence 394: Application US/10103313
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P12071
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 394
LENGTH: 144
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (86)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (87)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (106)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (111)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (113)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (114)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (142)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-394

```

| | | | | |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 29.48; | Score 577; | DB 6; | Length 144; |
| Best Local Similarity | 93.48; | Pred. No. 2.4e-44; | | |
| Matches 113; Conservative | 0; | Mismatches 8; | Indels 0; | Gaps 0 |

[illegible]

```

RESULT 6
US-10-103-313-379
; Sequence 379, Application US/10103313
; GENERAL INFORMATION:

```

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P0207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 379
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (146)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (164)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (171)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-379

Query Match 24.1%; Score 473; DB 6; Length 180;
Best Local Similarity 52.4%; Pred. No. 6.3e-35;
Matches 86; Conservative 33; Mismatches 37; Indels 8; Gaps 3;

QY 1 MANTSHADNIIQNLSP--LTAFKLTSLGFIIGSVNGMLISILVCKDTHRAPYF 58
DB 6 MANTGEPEEVSAGLSPSPASATYKLVLTGLIMCVSLAGNALLSLVLRALHRAKYF 65
QY 59 LLDCCSDILRSALICPEFVNSVKNSTWTYGLTCKVIAFLGVLSCEHTAFMLFCISVT 118
DB 66 LLDCLADGIRSAVCFEPVYASVRHGSSWTFSAISCKIVAFMAVLFCFHAFLMFCISVT 125
QY 119 RYLAIAHHRFYTKRLTFWTCLAVT-----CM-VWTLVSMAFPP 156
DB 126 RYMAIAHHRFYAKRMTLMTWCXAAAMXGPCLPMPFHLTLTWAP 169

RESULT 7
US-10-130-469-62
Sequence 62, Application US/10130469
GENERAL INFORMATION:
APPLICANT: Vogell, Gabriel
APPLICANT: Huff, Rita
APPLICANT: Sejlitz, Torsten
APPLICANT: Lind, Peter
APPLICANT: Slightom, Jerry
APPLICANT: Schellin, Kathleen
APPLICANT: Bannigan, Chris
APPLICANT: Ruff, Valerie
APPLICANT: Kayles, Paul
APPLICANT: Wood, Linda
APPLICANT: Parodi, Luis
APPLICANT: Hiebsch, Ronald
TITLE OF INVENTION: Novel G Protein Coupled Receptors
FILE REFERENCE: 237.PIUS
CURRENT APPLICATION NUMBER: US/10/130,469
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
CURRENT APPLICATION NUMBER: 60/166,071

PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: 60/186,811
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/188,114
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/190,310
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,800
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/201,190
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/203,111
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: 60/207,094
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-10-130-469-62

Query Match 23.9%; Score 470; DB 6; Length 143;
Best Local Similarity 58.5%; Pred. No. 9.2e-35;
Matches 83; Conservative 29; Mismatches 28; Indels 2; Gaps 1;

QY 1 MANTSHADNIIQNLSP--LTAFKLTSLGFIIGSVNGMLISILVCKDTHRAPYF 58
DB 1 MANTGEPEEVSAGLSPSPASATYKLVLTGLIMCVSLAGNALLSLVLRALHRAKYF 60
QY 59 LLDCCSDILRSALICPEFVNSVKNSTWTYGLTCKVIAFLGVLSCEHTAFMLFCISVT 118
DB 61 LLDCLADGIRSAVCFEPVYASVRHGSSWTFSAISCKIVAFMAVLFCFHAFLMFCISVT 120
QY 119 RYLAIAHHRFYTKRLTFWTCLAVT-----CM-VWTLVSMAFPP 156
DB 121 RYMAIAHHRFYAKRMTLMTWCXAAAMXGPCLPMPFHLTLTWAP 169

RESULT 8
US-10-130-469-30
Sequence 30, Application US/10130469
GENERAL INFORMATION:
APPLICANT: Vogell, Gabriel
APPLICANT: Huff, Rita
APPLICANT: Sejlitz, Torsten
APPLICANT: Lind, Peter
APPLICANT: Slightom, Jerry
APPLICANT: Schellin, Kathleen
APPLICANT: Bannigan, Chris
APPLICANT: Ruff, Valerie
APPLICANT: Kayles, Paul
APPLICANT: Wood, Linda
APPLICANT: Parodi, Luis
APPLICANT: Hiebsch, Ronald
TITLE OF INVENTION: Novel G Protein Coupled Receptors
FILE REFERENCE: 237.PIUS
CURRENT APPLICATION NUMBER: US/10/130,469
CURRENT FILING DATE: 2002-05-16

PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: 60/186,811
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/188,114
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/190,310
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,800
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/201,190
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/203,111
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: 60/207,094
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 106
TYPE: PRT
ORGANISM: Homo sapiens
US-10-130-469-30

Query Match 17.2% Score 337.5; DB 6; Length 106;
Best Local Similarity 59.2%; Pred. No. 5.1e-23;
Matches 61; Conservative 13; Mismatches 28; Indels 1; Gaps 1;
QY 250 GPTPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFLLTLMGPYLVACYWRY 309
DB 1 GMPPTLLGIRONGHAA-S-RLLGMDVEKGEKLGSRMFVITLTLFLLMSPYLVACYWRY 59
QY 310 FARGPVPCGFLTAAMWMSFAQAGINPVCIFSNRELRCFST 352
DB 60 FVKACAVPHRYLATAVWMSFAQAAVNPVYCFLLNKDKLCIRT 102
RESULT 9
US-10-176-255-31
Sequence 31, Application US/10176255
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Russo, Joseph F.
APPLICANT: Thomsen, William J.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human Serotonin Receptor
FILE REFERENCE: AREN-0328
CURRENT APPLICATION NUMBER: US/10/176,255
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 09/060,188
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 09/767,013
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/292,072

PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 478
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-10-176-255-31

Query Match 13.5% Score 264.5; DB 6; Length 478;
Best Local Similarity 23.9%; Pred. No. 8.4e-16;
Matches 83; Conservative 61; Mismatches 153; Indels 51; Gaps 9;
QY 30 IIGVSVGNLLISILVNDKTLHRAVYFFLLDLCSDILRSACPPFVNSKNGSTWY 89
DB 84 VIILTIAGNLIIVMAVSEKTLQNTNTFLMSLAIDLGLVNPVSMITLTYGRPL 143
QY 90 GTLCKVIAFLGVLSCEFTAFMFCISVTRYLAIA---HHRFYKRLFTWCLAVICWY 145
DB 144 PSKLCVAVIYDLVLFSTASIMHLCAISDRYVAIQNPITHSRNSRTAKELIIA----V 199
QY 146 WTLVNAAF-PYLDVGYSTIREDOCTPQHRSTRANDSLGFMILLALLATOLVYIK 204
DB 200 TTISVIGSIMPLVFGLODSKVFKEGSLADNDNFVLIGSEVSEFPILTIMVITYELIYK 259
QY 205 L-----IFEVHDKRRMKP---VOFVAVAVSOMTFFPGASGOAANWLAGFGRTPTPL 256
DB 260 VLRRQALMLHGHTEEPGLSLDLKCKRN-----TAEBNSN----- 299
QY 257 LGIRONANTTGRRL-----VLDEFKMEKRISRMFYIMTFLLTLMGPYLVACYWRY 309
DB 300 ---PNDONARRRRKKRRPRGTQMGINNERKASKVGIYFELVWMCPEFIINIAV 355
QY 310 PAR---GPVYGGFLTAAMWMSFAQAGINPVCIFSNRELRCFSTTL 354
DB 356 ICKSCNEDYIGALLNFWWIGYLSAVNPVYTLFNKRYRAFSENYL 403

RESULT 10
US-10-176-255-25
Sequence 25, Application US/10176255
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Russo, Joseph F.
APPLICANT: Thomsen, William J.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human Serotonin Receptor
FILE REFERENCE: AREN-0328
CURRENT APPLICATION NUMBER: US/10/176,255
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 09/060,188
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 09/767,013
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/292,072
PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-176-255-25

Query Match 13.1% Score 258; DB 6; Length 470;
Best Local Similarity 24.7%; Pred. No. 3.2e-15;
Matches 89; Conservative 63; Mismatches 155; Indels 54; Gaps 12;

QY 30 IIGSVVGNLLISILVCKTLHRAPIYFLDLCCSDILRSALCEPFEVNSKNGSTWY 89
 Db 84 VIILTAGNLIIVMAVSELEKLNATNFILMSLAIDMLGLFVLMVSMILITLYGRWPL 143
 QY 90 GTLCKVIAFLGVLSCEFHAFMLFCISVTRYLAIA---HHRYTKRLFTWCLAVICW 145
 Db 144 PSKLCAMVILYLDVLFSTASIMHLCAISLDRYVAIQNP IHSRFSRSKAFKLKITA---V 199
 QY 146 WTLVSAMAP-PYLDVGYTSFIREDOCTFHHSFRANDS-LGFMILLAILLATQUL-VY 202
 Db 200 WTISVGISMPFVGLQDDSKVFEKSGCLLADNPFVLIGSFVSFFIPLTIVITVYCLTIY 259
 QY 203 L---KLIFVHRRKMKP---VOFVAASONTWTFHFGASGQAAMNLAEGFGPPPTL 256
 Db 260 VLRQAMLLHGTTEPPGLSLDFLCKCKRN-----TLEENSAN----- 299
 QY 257 LGRONANTTGRRL-----VLDEFKMKRISRMFYIMTFLTLMGPIVACWRY 309
 Db 300 ---PNODNARRKKKERRPGTMOAINNERAKKVLGIVFEVFLIMCPEFITINIMAV 355
 QY 310 FAR---GPVPGGFLTAAMWMSFAQGINPVCISNRELRCFSTTL 354
 Db 356 ICKESCNEVIGALLNVFWMIGLSSAVNPLYTTLFNKIRAFSNYL 403

RESULT 13
 US-10-166-101-8
 Sequence 8, Application US/10166101

GENERAL INFORMATION:
 APPLICANT: Weinsbank, Richard L.
 APPLICANT: Branchek, Theresa
 APPLICANT: Hartig, Paul
 TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
 FILE REFERENCE: 39318-C
 CURRENT APPLICATION NUMBER: US/10/166,101
 PRIOR FILING DATE: 2002-06-10
 PRIOR APPLICATION NUMBER: 09/246,075
 PRIOR FILING DATE: 1999-02-05
 PRIOR APPLICATION NUMBER: 08/483,222
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/117,006
 PRIOR FILING DATE: 1994-08-22
 PRIOR APPLICATION NUMBER: PCT/US93/00149
 PRIOR FILING DATE: 1993-01-08
 PRIOR APPLICATION NUMBER: 07/817,920
 PRIOR FILING DATE: 1992-01-08
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.0 - beta
 SEQ ID NO 8
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-166-101-8

Query Match 12.9%; Score 253.5; DB 6; Length 470;
 Best Local Similarity 24.8%; Pred. No. 8e-15;
 Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

QY 30 IIGSVVGNLLISILVCKTLHRAPIYFLDLCCSDILRSALCEPFEVNSKNGSTWY 89
 Db 84 VIILTAGNLIIVMAVSELEKLNATNFILMSLAIDMLGLFVLMVSMILITLYGRWPL 143
 QY 90 GTLCKVIAFLGVLSCEFHAFMLFCISVTRYLAIA---HHRYTKRLFTWCLAVICW 145
 Db 144 PSKLCAMVILYLDVLFSTASIMHLCAISLDRYVAIQNP IHSRFSRSKAFKLKITA---V 199
 QY 146 WTLVSAMAP-PYLDVGYTSFIREDOCTFHHSFRANDS-LGFMILLAILLATQUL-VY 202
 Db 200 WTISVGISMPFVGLQDDSKVFEKSGCLLADNPFVLIGSFVSFFIPLTIVITVYCLTIY 259
 QY 203 L---KLIFVHRRKMKP---VOFVAASONTWTFHFGASGQAAMNLAEGFGPPPTL 256

Db 252 ITYVL---TIKSLQKNTLC-----VSDLTRAKLASFR--LPQSSLSSEKLFQ 296
 QY 260 ---RONANTTGRRLVLDEFKMKRISRMFYIMTFLTLMGPIVACWRYFAR--- 312
 Db 297 RSHREGSYTGRR---TMOISNEQKACKVLGIVFEVFLVMMCPFITINIMAVICKESC 353
 QY 313 GPVPGGFLTAAMWMSFAQGINPVCISNRELRCFS 351
 Db 354 NEDVIGALLNVFWMIGLSSAVNPLYTTLFNKIRAFSNYL 392

RESULT 14
 US-10-127-940-3
 Sequence 3, Application US/10127940

GENERAL INFORMATION:
 APPLICANT: Kopin, Alan S.
 APPLICANT: Beinborn, Martin
 TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
 PEPTIDE HORMONE RECEPTORS
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 176 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FastSeq version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/127,940
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/076,510
 FILING DATE: 12 MAY 1998
 APPLICATION NUMBER: 08/570,157
 FILING DATE: 11-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00398/109002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/428-0200
 TELEFAX: 617/438-7045
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 STRANDEDNESS: Not Relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-10-127-940-3

Query Match 12.9%; Score 253; DB 6; Length 448;
 Best Local Similarity 24.9%; Pred. No. 8.5e-15;
 Matches 102; Conservative 47; Mismatches 146; Indels 114; Gaps 16;

QY 22 IKITSGLFIVGVGNLLISILVCKTLHRAPIYFLDLCCSDILRSALCEPFEVNSV 81
 Db 56 IRTTIAVIFLMSVGNMILYVLSRRLTYTNFLSLAVSDLLAVACHPTLLPN 115
 QY 82 KNGSTWYGLTCKVIAFLGVLSCEFHAFMLFCISVTRYLAIAHHRYTKRLFTWY 137
 Db 116 LMG-TFIFGVICKAVSYLMGVSVSYTSLVAIALERSAICR---PLQARVWQTRSH 170

Search completed: July 19, 2002, 14:40:32
J00 time: 128 sec

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OY 138 CLAVICWMTLSVMAAP-PVLDTGCTSYRRED-----OCTPHRSFRANDSLGFMLLTA 192
Db 171 AARVIVATWTLGLMLVPPV-----YTVQPVGPRVLCCVHRMPSARQWTSVLLLL 225
OY 193 LIL-----LATQLVYKLIF-----FVHRRKMPVQFV 221
Db 226 LFFTPGVMAVAAYGISRELVIYGLRFDGSDSDSQRVNRNCGLGPGAVHNGRCRPE--T 283
OY 222 AAVSON-----WTFHGPASGOAANMLAGFGGPTPTLLGIRON 262
Db 284 GAVGEDSDGCVQJLPRSPALELTALTAPGPGSGSR-----PTQAKLLA----- 328
OY 263 ANTGRRLLVLDERKMKRISRMVIMTFLETLMGPYLVACYWPFVARGP-----VVRG 318
Db 329 -----KKRVVRLVIVVFLCMLPVYSANTWRAP-DGPGARHALSG 370
OY 319 GFLTAAMWSFAQAGINPFCIFSNRELNR-CFSTTLICRKSRLPREP 366
Db 371 APISFHLSTASACVNPVLCFMRFRQACLETGARC-----PRPP 414
```

```
RESULT 15
US-60-380-336-52
; Sequence 52, Application US/60380336
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0262 PSP
; CURRENT APPLICATION NUMBER: US/60/380,336
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 470
; TYPE: PRP
; ORGANISM: Oryzias latipes
US-60-380-336-52
```

Query Match 12.9% Score 252.5; DB 7; Length 470;
Best Local Similarity 24.0%; Pred. No. 9,9e-15;
Matches 90; Conservative 64; Mismatches 160; Indels 61; Gaps 12;

```
OY 2 ANYSHADNIIQNLSPLETAFLKLSIGFLIGY-----SVGNLLISILVYKDKTLHRAPY 57
Db 11 SNCSHV-----LAPELNTYKAVVGLGVLGFILEGVIGNILVILSVYCHRLQTVTY 63
OY 58 FLDDICCDILRSALCFPP--VENSVKNGSTWTYGLTKVTAFLGVLSCFHTAFMLFCI 115
Db 64 FIVNLAVALDLLSTVLPFSAIFEIL---DRWVFGRFVFCNMAADVLCCTASIMSLCVI 120
OY 116 SVTRFLAIAHREYTKRLFEWTCCLAVICWMTLSVMAAPPVL-----DVGYSFIRE 168
Db 121 SVDRYIGSVYPRPAIMTKRALAAMLWLVLSIIGLPGKKEPADEDTVCKITE 180
OY 169 EDOCTFOHRSFRANDSLGFMLLALATOLVYKLIFVHRRKMKPVQFAAVSQNW 228
Db 181 EP---GAIFSAVGS--FYLPALIIILAMYCRYV-----VAQKESRG 217
OY 229 TFHGPASGOAANMLAGFGGPTPTLLGIRONANTTGRRLLVLDERKMKRISRMV 288
Db 218 LKEGQIKESDSEQVILRHHRGNTVS---EDEALRSRTHFALRLKFSREKKAKTG 273
OY 289 IMTFLEFLMGPYLVACYWPFVARGPVG-----GFLTAAMWSFAQAGINPFCIFSN 343
Db 274 IIVGCFVLCMLPFEL-----VLPIGSIIPAPYPSDTEVKITFVLGTFNSCINPIITLCSN 328
OY 344 RELRCFSTTL-LYC 357
Db 329 QEFKKAFOSSLGVMC 343
```


| Accession | Sequence | Length |
|-----------|-------------------------------------------------------------|--------|
| Db | ANWLAGEGREGTPTLLIGINQNNANTGRRRLVLDPEKKMKRISRMFVIMTFLEFLIMGP | 300 |
| Qy | YLVACYNRVNFRGSGVYGGFLLTAAYMMSPFAQAGINPVCISNRRLRRCFSTLLYCRSS | 360 |
| Db | YLVACYNRVNFRGSGVYGGFLLTAAYMMSPFAQAGINPVCISNRRLRRCFSTLLYCRSS | 360 |
| Qy | RLRPREPYCVI 370 | |
| Db | RLRPREPYCVI 370 | |

RESULT 2
JC7289
G-protein coupled receptor, SREB3 - human
C.Species: Homo.sapiens (man)
C.Date: 18-Aug-2000 #sequence_rev: 18-Aug-2000 #text_change 02-Sep-2000
C.Accession: J07289
R.Matsumoto, M.; Salto, T.; Takasaki, J.; Kamohara, M.; Sugimoto, T.; Kobayashi, M.; Tachibana, H.; Ohno, S. Biochem. Biophys. Res. Commun. 272, 576-582, 2000
A.Title: An evolutionarily conserved G-protein coupled receptor family, SREB, expressed in the developing mouse brain.
A.Reference number: J07287
A.Accession: J07289
A:Molecule type: mRNA
A:Residues: 1-373 <MAT>
C:Cross-references: DDBJ:AB040799
C:Genetics:
A:Gene: srebb3
A:Map position: Xp11
C:Keywords: Brain; G protein-coupled receptor; glycolysis; reproduction; transmembrane protein

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 65.48; | Score 1283.5; | DB 2; | Length 373; |
| Best Local Similarity | 62.38; | Pred. No. 4.8e-108; | | |
| Matches 233; | Conservative 56; | Mismatches 80; | Indels 5; | Gaps 3 |

Db 1 MAINTGEPEEVS GALSPPSASAYVKLVLLGLIMCVSLAGNAIILSLVLKERALHAPYF 60

```

Oy      59 LDDCCSDILSAICPPFVENVSKNGSWTGYGLTCKVAFLGVUSCFHFAFMFCISVT 118
        |||| : ||||| ||| :|||: ||| :||| ||| ||| ||| ||| |||
Db      61 LDDCLADGIRSAVCFPVLASVRHGSSWTFSAISCKIYAEMAVLECFHFAFMFCISVT 120

```

Db 121 RYAAIAHHFRFAKRMTLWICAAVICMAWTLISVAMAPRPVEDVGTYKFIREDQCIFEHRY 180

Db 181 FRANDTGFMLAVLMATHAVYKLLFEYRHRMRKPVOVMRAISOONTIEHGPATGO 240

[illegible]

Db 300 SPYVACVWRVEFKACAVPHRYLATVWMSFAQAAVNPVCFLLNKDKLCRLTHAPCWG 359

357 CAGGAGGAGGCTCT 370
 : |||||:
 360 TGGAGAPRPPYCV 373
 Db

RESULT 3
JC7287

C/Species: *nomio sapientis* (man)
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C/Accession: J07287

A>Title: An evolutionarily conserved G-protein coupled receptor family, SREB, expressed

A:Reference number: JC7287
A:Accession: JC7287
A:Molecule type: mRNA
A:Residues: 1-375 <Mat>
A:Cross-references: DDBJ:AB040799

A;Map position: 3p21-14
C;Keywords: brain; glycolysis; reproduction; transmembrane protein

| | | | | |
|---------------------------|-------|-------------------|----------|------------|
| Query Match | 50.9% | Score 998.5 | DB 2 | Length 375 |
| Best Local Similarity | 55.2% | Pred. No. 2.4e-82 | | |
| Matches 190; Conservative | 51 | Mismatches 96 | Indels 7 | Gaps 3 |

Qy 22 LKLTSGFIIGSVGNLLISILVKDKTHRAPYFLDLDCSDILRAICFPFVNSV 81
|| : || : || : || : || : || : || : || : || : || : || : || :
Db 20 LKIATISLLTCSLAGNLFALLIVERSLHAPRYLLDLCADGLRALACLPAVMLEA 79

```

QY      82 KNGSWT---YGTLPCKVIAFGVLSCHTAEMFCISVTRYLAIAHHRFYTKRLFTWTC 138
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      80 RRAAAGAGPAGALGCKLLAFLAALFCHAAFLGLGVTRYLAIAHHRFYAERLGGWPC 139

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QY      139  LA-VICMWTLISVAMAFPPVLDVGTYSIREEDQCTPQHSFRADSLGFMILLALILLA 197
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      140  AAMLCVAAWALALAAAFPPVLIDGGDD--EDAPCALIQRPDGGAGALGFLILLAVVGA 196

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QY 198 TQLYVTKLFFVHDRKKMKPVQVFAANVSQNWTFHFGPGASQAAAANWLAGFGRGPTPTLL 257
 . | | | | : | | | | | : | | | : | | | | | | | | | | | | :
 DB 197 THLVYLRLEFFIHDRRKMRLVPAVSHDWTFFHGGATGQAAAANWTAGFGRGPTPALV 256

```

QY 258 GIRQNANTTGGRRLLVDEEFKEKRISMFIYIMFLFLIMGPVLVACYMKVFAFGVVP 317
    |||  |||:|||||: |||: ||| |||||:| |||  ||
DB 257 GIRPAGPGRGARLLVLEEFKEKRLCMFYAVLLFLIMGPYVVASYLEVLVBPQAVP 316

```

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QY 318 GGFLLTAVMNMFPAQAGINPVCISNRELRCRSTLLYCRSR 361
      :||:||||:|||||:-|| ||||| || :|
DB 317 QAYLLTASVWLTFPAQAGINPVCLEFNRELRLDCEPAQPCQCSER 360

```

RESULT 4
JC5042
G protein-coupled receptor - harnac

C:Species: Balanus amphitrite (barnacle)
C:Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000
C:Accession: JC5042
B:Food: A. Tenebrion. H. Olerobr. V. Chiron. V.

Gene 175, 95-100, 1996
A>Title: Molecular cloning of a new member of the putative G protein-coupled receptor
A | Reference number: JCS042; MUID:970704655
A | Accession: JCS042
A | Accession: JCS042

A: Molecule type: DNA
A: Residues: 1-476 <ISO>
A: Cross-references: DDBJ: g1514430; PIDN: BAA11375.1; PID: g1514431
C: Subcellular localization: cytoplasm, mitochondrion
C: Subcellular localization: cytoplasm, mitochondrion

C/Keywords: G-protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F.34-5/Domain: transmembrane #status predicted <TM1>
F.71-93/Domain: transmembrane #status predicted <TM2>
F.107-129/Domain: transmembrane #status predicted <TM3>

| | | |
|------------------|-------------------|------------------------|
| F:126-134/Region | G protein-binding | #status predicted |
| F:148-172/Domain | transmembrane | #status predicted <TM> |
| F:199-222/Domain | transmembrane | #status predicted <TM> |
| F:272-280/Domain | transmembrane | #status predicted <TM> |

F-407-430/Domain: transmembrane #status predicted <TM>
F-13_17/Binding site: carboxylate (Asn) (covalent)
F-250_240,250,260/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM>

| Query Match | Score | DB 2 | length |
|-----------------------|-------|------|--------|
| 13.1% | 257.5 | | 476 |
| 21.6% | | | |
| Best Local Similarity | 26.15 | | |

[illegible]

QY 8 ADNLQNLSTPLTAF-----LKTSLGFIGSVGNLLISILVYKDKTLHAPRY 57
 Db 11 ADNVLNWSGCRPATLFDMDRHLISLALANLWVAGNLLVNAVFNHSLRTVTNL 70
 QY 58 FLILDCSDILRSALCFPFVFNKSGSTWTGTLTKCIAFLAGVSCFETAPMLFCISV 117
 Db 71 FIVSLACADLVGLMVLPR-SATLEVLVDVLYGDVWCSTWLANVDMKSSILNLCAISL 129
 QY 118 TRYLAIAHRRFYTKRLTEWTCIAVICMWTLSVMAAFPPVLD---VGTFSTREDDQCT 173
 Db 130 DRYLAVSOPISYPSLMSSTRAKOLIAAVWVLSFVICFPPLVGMNDPRGTLISGSGSACR 189
 QY 174 F-----QHRSEFANDSLGEMLLALILATOLVYLKLIFFVHDRKMKPQFPAVNSQM 228
 Db 190 LTCLELNERGYIYALSSEFLPSTVM-----FFGRIYRTAVSTTRALAQGR 238
 QY 229 -----GFGGASQOAAANMLA---245
 Db 239 RTTKDESGRLTLRIHGRSVYQRAEQAAAGARAHGVRLLISEGARRQNKPSFVHC 298
 QY 246 -----GFGP-----GPTPTLLG---IRON 262
 Db 299 REDSRAKNOYEIYVEGSGRGRVPOQRPDAKLSSASQSESDSRPRFISRSRN 358
 QY 263 ANTGRRLVLDERKMKRISRMFYIMTFLLTLTGPIVACVRYEARG---PVVPGG 319
 Db 359 VRHQARR-----FRMETKAKATGIIYGLFLLCMLPFEV-CY---LVKFGCADCVPPL 407
 QY 320 FLTAAVMSFPAAGINPVCIFSNRELRCFSTTL--LTCRSRLPR 364
 Db 408 LPSVFWLGYCNSAVNPCVYALCSRDEFRAFSSILCKCVRGAMER 454

RESULT 5

A43956
 N:Alternatn names: 5-hydroxytryptamine receptor 2A (5-HT2A)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
 C:Accession: A43956; J50615; I56514
 R:Chen, K.; Yang, W.; Grimsby, J.; Shih, J.C.
 Brain Res. Mol. Brain Res. 14, 20-26, 1992
 A:Title: The human 5-HT2 receptor is encoded by a multiple intron-exon gene.
 A:Reference number: A43956; MUID:92356792
 A:Accession: A43956
 A:Molecule type: DNA
 A:Residues: 1-471 <CH2>
 A:Cross-references: GB:542168; NID:9252946; PIDN:AAE22791.2; PID:95705962
 A:Experimental source: normal lymphoblast cell line
 A:Note: the authors translated the codon CCA for residue 405 as Thr and CCG for residue
 R:Saltman, A.G.; Morse, B.; Whitman, M.M.; Ivanschchenko, Y.; Jaye, M.; Felder, S.
 Biochem. Biophys. Res. Commun. 181, 1469-1478, 1991
 A:Title: Cloning of the human serotonin 5-HT2 and 5-HT1C receptor subtypes.
 A:Reference number: J50615; MUID:92109767
 A:Accession: J50615
 A:Molecule type: mRNA
 A:Residues: 1-471 <SAL>
 A:Cross-references: GB:X57830; NID:936430; PIDN:CAA40963.1; PID:936431
 R:Cook, E.H.
 J. Neurochem. 63, 465-469, 1994
 A:Title: Primary structure of the human platelet serotonin 5-HT2A receptor: identify wit
 A:Reference number: I56514; MUID:94308772
 A:Accession: I56514
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-471 <RES>
 A:Cross-references: GB:S71229; NID:9547295; PIDN:AAE31320.1; PID:9547296
 C:Comment: This protein is associated with vascular contraction and platelet aggregation
 C:Genetics:
 A:Gene: GDB:HTR2A; HTR2
 A:Cross-references: GDB:125192; OMIM:182135
 A:Map position: 13q14-13q21

A:Introns: 138/1: 205/1
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tra
 F:75-100/Domain: transmembrane #status predicted <TM>
 F:111-132/Domain: transmembrane #status predicted <TM>
 F:148-170/Domain: transmembrane #status predicted <TM>
 F:192-213/Domain: transmembrane #status predicted <TM>
 F:234-254/Domain: transmembrane #status predicted <TM>
 F:326-346/Domain: transmembrane #status predicted <TM>
 F:363-384/Domain: transmembrane #status predicted <TM>
 F:38,44,51,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 253.5; DB 2; Length 471;
 Best Local Similarity 24.8%; Pred. No. 4,5e-15;
 Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

QY 30 IIGSVVGNLLISILVYKDKTLHAPRYFLILDCSDILRSALCFPFVFNKSGSTWTY 89
 Db 84 VILITAGNLTIVMAVSLERKLNATNYPFLMSLAIDMLGFLVPMVSMILITGYRML 143
 QY 90 GTLCKVIAFLGVLSCHFTAFMLFCISVTRIAIA-----HHRFYTKRLTFWTCIAVICM 145
 Db 144 PSKLCVAVIYLDVLFSTASIMHLCALSLDRVVALQNPVHHSRNSKTKAFIKITA----V 199
 QY 146 WLSVMAAF-PVLDVGTYSFIREDDQCTEQHRSFRANDSLGEMLLALILATOLVYLK 204
 Db 200 WTSVGSIMPIPVFGIIDDKVFRESCLL-----ADDN--FVLISFVSFFIPIITMV 251
 QY 205 LIFVHDRMRKPVQFAAVNSQMTFHPGASQOAAANMLAGFGRGPTPTLLGI----- 259
 Db 252 ITYFL-----TIKSLQKATLC-----VSDIGTRAKLASFSF--LPQSSLSSEKLFQ 296
 QY 260 -----RONANTGRRLVLDEPFKMKRISRMFYIMTFLLTLTGPIVACVRYEAR-- 312
 Db 297 RSHREPGSTYGR--TWQISNEQACVYLGIVFVVMCPFTTINMAVICKESC 353
 QY 313 GPVPPGGFLTAAVMSFPAAGINPVCIFSNRELRCFS 351
 Db 354 NEVIGALLNVFVWIGVIGLSSAVNPVLTTLNKKYRSFAS 392

RESULT 6

S11280
 N:Alternatn names: 2-Chinese hamster
 C:Species: Cricetus griseus (Chinese hamster)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
 C:Accession: S11280
 R:Chamhard, J.C.; van Obergerhen-Schilling, E.; Haslam, R.J.; Vouret, V.; Pouyssegur,
 Nucleic Acids Res. 18, 5282, 1990
 A:Title: Chinese hamster serotonin (5-HT) type 2 receptor cDNA sequence.
 A:Reference number: S11280; MUID:90384833
 A:Accession: S11280
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-471 <CH2>
 A:Cross-references: EMBL:X53791; NID:949455; PIDN:CAA37800.1; PID:949456
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.9%; Score 253; DB 2; Length 471;
 Best Local Similarity 24.4%; Pred. No. 4,9e-15;
 Matches 86; Conservative 67; Mismatches 150; Indels 50; Gaps 13;

QY 30 IIGSVVGNLLISILVYKDKTLHAPRYFLILDCSDILRSALCFPFVFNKSGSTWTY 89
 Db 84 VILITAGNLTIVMAVSLERKLNATNYPFLMSLAIDMLGFLVPMVSMILITGYRML 143
 QY 90 GTLCKVIAFLGVLSCHFTAFMLFCISVTRIAIA-----HHRFYTKRLTFWTCIAVICM 145
 Db 144 PSKLCVAVIYLDVLFSTASIMHLCALSLDRVVALQNPVHHSRNSKTKAFIKITA----V 199

[illegible]

N:Alternate names: 5-hydroxytryptamine receptor 2 (5-HTR2)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Dec-1969 #sequence_revision 01-Dec-1989,#text_change 13-Aug-1999
C:Accession: S02011
R:Pritchett, D.B.; Bach, A.W.J.; Wozny, M.; Taleb, O.; Dal Toso, R.; Shih, J.C.; Seet
EMBO J. 7, 4135-4140, 1988
A>Title: Structure and functional expression of cloned rat serotonin 5HT-2 receptor.
A:Reference number: S02011, MUID:69210797
A:Accession: S02011
A:Molecule type: mRNA
A:Residues: 1-449 <PR>
A:Cross-references: EMBL:X13971; NID:g57855; PIDN:CAA32150.1; PID:g57856
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.7%; Score 250; DB 2; Length 449;
Best Local Similarity 24.1%; Pred. No. 8-8e-15;
Matches 85; Conservative 67; Mismatches 131; Indels 50; Gaps 13;

OY 30 IIGVAVGNLLISILVKKDTLHRAVYFLDLCSSDLISAICPEPVNSVKNGSTWTY 89
 ::::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 62 VILLIAGNIIVIMAVSLEKIKQNTATNYELMSLAIDLMLGLVLVPVSMITLVGYRPL 121
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 90 GTLTCKVAIFAGVLSCFITAFMFCISTRTIALA----HHRFYTKRLTFMTCLAVICMY 145
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 122 PSKDCIAIITYLDVFETSTASIMHLCAISLDRYVAIONPIHSHNFNSRTAPFLKIIA---V 177
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 146 WTLSAAVAF-P-VLDVGVTYSFIREDDCTPQHRSFRANDSGFMALLAILLATQLYYLK 204
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 178 WTISGISMPIPFVEILODSKYFKKGSCLL-----ADDN--FVLISGFVAFPIPTIMV 229
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 205 LIEFYHDRKKMKPVQFAVASQMTFHFGPGASGAANAMNLAGEFGRPPTLLGI----- 259
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 230 ITTYFL----TKISLOKEATLC-----VSDLSTRAKLASFSF--LPQSLSSEKLQ 274
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 260 ----KQNANTTGRRRLVLDFEFKMEKRISRKFYITMFLEFILMGVYLACWVRPAR--- 312
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 275 RSIHREPSTYAGR--TMOGISNEOKACKYLGIVFFLEFVMVCFFTINIMAYICKESC 331
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 332 NENVIGALLNVFWIGYSSAVNPVLVTLENKTRSAFS-RTIQCYENRKRP 383
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
JC2459
gastrin/cholecystokinin B receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Apr-2000
C:Accession: JC2459
R:Blandlitz, C.; Song, I.; Yamada, T.
Biochem. Biophys. Res. Commun. 202, 947-953, 1994
A>Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptc
A:Reference number: JC2459; MUID:94324990
A:Accession: JC2459
A:Molecule type: mRNA
A:Residues: 1-452 <BLA>
A:Cross-references: GB:L31548; NID:g495663; PIDN:AAA31194.1; PID:g495665
C:Genetics:
A:Introns: 49/1; 133/1; 216/2; 273/1
C:Superfamily: neurokinin 1 receptor
C:Keywords: receptor; transmembrane protein.
F:56-79/Domain: transmembrane #status predicted <TM1>
F:85-104/Domain: transmembrane #status predicted <TM2>
F:130-149/Domain: transmembrane #status predicted <TM3>
F:169-187/Domain: transmembrane #status predicted <TM4>
F:217-237/Domain: transmembrane #status predicted <TM5>
F:339-359/Domain: transmembrane #status predicted <TM6>
F:381-400/Domain: transmembrane #status predicted <TM7>

Query Match 12.7%; Score 249; DB 2; Length 452;

Query Match

12.78; Score 249; DB 2; Length 452;

Best Local Similarity 25.0%; Pred. No. 1,1e-14;
Matches 100; Conservative 52; Mismatches 158; Indels 90; Gaps 15;

OY 22 LKLSIGFICGVSVNLLISILVKDKTLHRAPIYFLDLCCSDILRSACEPVENSV 81
Db 54 IRTTLAVFELMSVGNILIVLGLSRRLRTVNAFLLSLAVSDLLAVACMEFTLLPN 113
OY 82 KNGSPTVCTGLCKVIAFLGSCFHTAFMLFCISVTRYALAHNRRTYRLTFWT---- 137
Db 114 LMG-FFIFETVICKAVSYLMGVSVSTSLVAIALERSALICR---PLQARVQWRSH 168
OY 138 CLAVICMWTLSSVAAAF-PVLDVGYTSFIREED---OCTFOHRSFRANDSLGFMELLA 192
Db 169 AARVILATFLLSGLLMVPV-----YFVQPVGPRLQCVHMRPSARVQWVSVLLLL 223
OY 193 LIL-----LATQLYVKLIF-----VHRRKMK 216
Db 224 LFFVDPVAAVAVAGLISRELTLDFDSDSESQSRVRCGGILPGAGAPVHONRCR 283
OY 217 PVQFVAAVSQNTF-----HGPGASGOAANMLAGRGPTPTLLGIRONANTTGRRL 271
Db 284 PEAGLAGEDGCCYVLPSPRPLELSALTAPISGPGPGRP-----AQAKL 330
OY 272 LVLDKEMKMRISRMFYIMTFLETLMGPYLVACYMVFARGP---VDPGFLTAVM 327
Db 331 LA-----KKRYRMILVIVLEFPMCLPYVSANTPRAF-DGFGARALSGAPISFIHL 383
OY 328 SFAAGINPFCIFSRELRR-CEFTLLLYCRKSRRLPREP 366
Db 384 SYASACVNPVLYCCFMHRRFROACLDTCARCC-----PRPP 418

RESULT 10

S40689
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S40689
R:Yang, W.; Chen, K.; Lan, N.C.; Gallaher, T.K.; Shih, J.C.
J. Neurosci. Res. 33, 196-204, 1992
A:Title: Gene structure and expression of the mouse 5-HT2 receptor.
A:Reference number: S40689; MUID:93085774
A:Accession: S40689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-471 <YAN>
A:Cross-references: EMBL:S49542; NID:g261074; PIDN:AAB24369.1; PID:g261075
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.7%; Score 249; DB 2; Length 471;
Best Local Similarity 23.1%; Pred. No. 1,1e-14;
Matches 83; Conservative 65; Mismatches 148; Indels 64; Gaps 12;

OY 30 IIGSVVGNLLISILVKDKTLHRAPIYFLDLCCSDILRSACEPVENSVNGSTWTY 89
Db 84 VILLIAGNIIIVMAVSEKRLQNTNPFILMSLAIDMLGFLVMEVSMITIIYGRMPL 143
OY 90 GLTCKVIAFLGVLSCFHTAFMLFCISVTRYALA---HHREYTRKLTFTWCLAVICW 145
Db 144 PSKLCAMVITLDVLFSTASIMHLCALISDRVAIQNPFIHSRNSKTKAFKITA---V 199
OY 146 WTLSSVAAAF-PVLDVGYTSFIREDOCTFOHRSFRANDSLGFMELLALATOLVYLK 204
Db 200 WTISGISMPIPVFGLODSKVFEGSCLL---ADON--FVLIGSFVAFIPIPLTIW 251
OY 205 LIF-----VDRKMKRVQVVAAVSQWMTTHGPGASGOAANMLAGRG 248
Db 252 ITYFLLTISLQKATLCVSDLSSTRAKLSFSFL-----POSSLSSEKTLFORSIH 300
OY 249 RGPFPPTLLGIRONANTTGRRLVLVDKEMKMRISRMFYIMTFLETLMGPYLVACYMR 308

Db 301 REP-----GSYAGR---TMSISNBQKCKVIGVIFLFLVVMKCFEITINMA 346
OY 309 VFAR---GVPVPGFLTAAMVMSFAQAGINPFCISNRELRCSTLLYC--RKRSLP 363
Db 347 VICRESNENIGALLANFVWIGYLSAVNPLVYTLFPKRTSARS-RYIOQYKENRP 405

RESULT 11

S28058
serotonin receptor 5 - mouse
N:Alternate names: 5-hydroxytryptamine 5 receptor (5HT₂-5)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C:Accession: S28058
R:Plassart, J.L.; Boscher, U.; Amalaky, N.; Hen, R.
EMBO J. 11, 4779-4786, 1992
A:Title: The mouse 5HT₂ receptor reveals a remarkable heterogeneity within the 5HT₂D
A:Reference number: S28058; MUID:9309851.
A:Accession: S28058
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <PLA>
A:Cross-references: EMBL:218278
C:Superfamily: octopamine receptor type I
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tra

Query Match 12.7%; Score 248.5; DB 2; Length 357;
Best Local Similarity 24.6%; Pred. No. 9.4e-15;
Matches 87; Conservative 56; Mismatches 151; Indels 59; Gaps 12;

OY 18 LTAFL-KLTSIGFICGVSVNLLISILVKDKTLHRAPIYFLDLCCSDILRSACEP 75
Db 36 LSAFRLVLETLGLFLAATFTMLLVLATILKVFTRHVRPNHVAASMAISDLVAVLVMP 95
OY 76 FVFSVANGSMTWTGTLCKVIAFLGSCFHTAFMLFCISVTRYALAHNRFTYRLTF 135
Db 96 LSLVHELSGRWQGRRLQQLIMADVLCCTASIMNVAIALDRWSTIRHLEYTLRTRK 155
OY 136 WTCIAVICMWTLSSVAAAF-PVLDVGYTSFIREDOCTFOHRSFRANDSLG-FMELL 191
Db 156 RVSNVMLLTMALSTVLSLAPL-FGMEYTSSESEQVS-REPSYVSTVGAFYPL 213
OY 192 ALILATQLYLKLIFVHDR--KMRPVQFVAAVSQWMTTHGPGASGOAANMLAGRG 249
Db 214 CVVLEFVWKIYBAKFRGSKTNSVPEAVEY-KNATQH----- 254
OY 250 GPPPTLLGIR-----QNAFTGRRLVLVDKEMKMRISRMFYIMTFLETLMGPYLV 303
Db 255 ---PQWFTVRHATVTPQTEGDTRRE-----QKEORALAMGILIGVFLCMFPFV 303
OY 304 A-----CYMRVFAFGPVPGFLTAAMVMSFAQAGINPFCISNRELRCF 350
Db 304 TELISPLCSMD-----VPAIMKSIPLWIGYSFENPLIYTAFNRSYSAF 349

RESULT 12

A47430
gastrin/cholecystokinin receptor B, short splice form - human
N:Alternate names: CCK-B/gastrin receptor; cholecystokinin-B/gastrin receptor
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A47430; JCI352; A46645; A48262
R:Ito, M.; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.; Nakata, J. Biol. Chem. 268, 18300-18305, 1993
A:Title: Functional characterization of a human brain cholecystokinin-B receptor. A
A:Reference number: A47430; MUID:93352657
A:Accession: A47430
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-447 <TTO>
A:Cross-references: GB:D13305; NID:g436039; PIDN:BAA02564.1; PID:g436040
A:Experimental source: brain

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OM protein - protein search, using sw model

Run on: July 19, 2002, 14:39:39 ; Search time 13.42 seconds

(without alignments)
1067.529 Million cell updates/sec

Title: US-09-698-419-14

Sequence: 1663
1 MANYSHADNIQNLSPFLTA.....STLLKCRSRRLREPRVCVI 370

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1963 | 100.0 | 370 | 1 | GP85_HUMAN |
| 2 | 1865.5 | 95.0 | 371 | 1 | GP85_BRARE |
| 3 | 1339.5 | 68.2 | 387 | 1 | SRB3_BRARE |
| 4 | 1283.5 | 65.4 | 373 | 1 | SRB3_HUMAN |
| 5 | 1276.5 | 65.0 | 373 | 1 | SRB3_RAT |
| 6 | 998.5 | 50.9 | 375 | 1 | GP85_HUMAN |
| 7 | 989 | 50.4 | 377 | 1 | GP85_RAT |
| 8 | 989 | 50.4 | 379 | 1 | GP85_MOUSE |
| 9 | 257.5 | 13.1 | 453 | 1 | CCR_XENLA |
| 10 | 257.5 | 13.1 | 476 | 1 | CCR_XENLA |
| 11 | 253.5 | 12.9 | 471 | 1 | SH2A_HUMAN |
| 12 | 253.5 | 12.9 | 471 | 1 | SH2A_MOUSE |
| 13 | 253 | 12.9 | 471 | 1 | SH2A_CRICR |
| 14 | 252.5 | 12.9 | 400 | 1 | OPN3_MOUSE |
| 15 | 252.5 | 12.9 | 470 | 1 | ALIA_ORYLA |
| 16 | 251.5 | 12.8 | 388 | 1 | SH4_CAVPO |
| 17 | 251.5 | 12.8 | 470 | 1 | SH4_MOUSE |
| 18 | 251 | 12.8 | 470 | 1 | SH2A_PIG |
| 19 | 250 | 12.7 | 471 | 1 | SH2A_RAT |
| 20 | 249 | 12.7 | 452 | 1 | SH2A_RAT |
| 21 | 249 | 12.7 | 471 | 1 | SH2A_MOUSE |
| 22 | 248.5 | 12.6 | 447 | 1 | SH2A_MOUSE |
| 23 | 247.5 | 12.5 | 447 | 1 | SH2A_MOUSE |
| 24 | 244.5 | 12.4 | 428 | 1 | SH2A_MOUSE |
| 25 | 244 | 12.4 | 428 | 1 | SH2A_MOUSE |
| 26 | 243.5 | 12.4 | 388 | 1 | SH4_HUMAN |
| 27 | 243 | 12.4 | 452 | 1 | SH4_HUMAN |
| 28 | 243 | 12.4 | 452 | 1 | SH4_HUMAN |
| 29 | 242.5 | 12.4 | 357 | 1 | SH4_HUMAN |
| 30 | 241.5 | 12.3 | 436 | 1 | SH2C_MOUSE |
| 31 | 241.5 | 12.3 | 436 | 1 | SH2C_MOUSE |
| 32 | 241 | 12.3 | 458 | 1 | SH2C_MOUSE |
| 33 | 239.5 | 12.2 | 357 | 1 | SH5A_HUMAN |

| | | | | | |
|----|-------|------|-----|---|------------|
| 34 | 238 | 12.1 | 539 | 1 | DOP2_DROME |
| 35 | 237.5 | 12.1 | 515 | 1 | ALIA_MESAT |
| 36 | 237 | 12.1 | 467 | 1 | BIAR_BOVIN |
| 37 | 236 | 12.0 | 454 | 1 | BIAR_BOVIN |
| 38 | 236 | 12.0 | 459 | 1 | SH2C_MOUSE |
| 39 | 235.5 | 12.0 | 453 | 1 | SH2C_MOUSE |
| 40 | 235 | 12.0 | 446 | 1 | SH7_CAVPO |
| 41 | 235 | 12.0 | 466 | 1 | SH7_CAVPO |
| 42 | 234.5 | 11.9 | 387 | 1 | BIAR_RAT |
| 43 | 234.5 | 11.9 | 392 | 1 | BIAR_RAT |
| 44 | 233.5 | 11.9 | 402 | 1 | BRSA_BOMOR |
| 45 | 233.5 | 11.9 | 406 | 1 | OPN3_HUMAN |

ALIGNMENTS

| RESULT | ID | GP85_HUMAN | STANDARD | PRT | 370 AA. |
|--------------------|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|-----|---------|
| AC | 09NPDI | 09NPDI | | | |
| DT | 16-OCT-2001 | (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 | (Rel. 40, Last sequence update) | | | |
| DT | 16-OCT-2001 | (Rel. 40, Last annotation update) | | | |
| DE | | Probable G-protein-coupled receptor GPR85 (Super conserved receptor expressed in brain 2) (P6RCX1). | | | |
| DE | | GP85 OR SREB2. | | | |
| GN | | GP85 | | | |
| OS | | Homo sapiens (Human), and Mus musculus (Mouse), and Rattus norvegicus (Rat). | | | |
| OS | | Rattus norvegicus (Rat). | | | |
| OC | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| NCBI | | TaxID=9606, 10090, 10116; | | | |
| NCBI | | TaxID=9606, 10090, 10116; | | | |
| SEQUENCE FROM N.A. | | | | | |
| RC | | SPECIES-Human, and Mouse; SPRAIN-CD-1; TISSUE-Fetal brain, and Brain; MEDLINE-20435311; PubMed-10978537; | | | |
| RA | | Heliebrand S., Schaller H.C., Wittenberger T.; "The brain-specific G-protein coupled receptor GPR85 with identical protein sequence in man and mouse maps to human chromosome 7q31."; | | | |
| RL | | Biochim. Biophys. Acta 1493:269-272(2000). | | | |
| SEQUENCE FROM N.A. | | | | | |
| RC | | SPECIES-Human, and Rat; TISSUE-Brain; MEDLINE-20294882; PubMed-10833454; | | | |
| RA | | Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.; "An evolutionarily conserved G-protein coupled receptor family, SREB, expressed in the central nervous system."; | | | |
| RL | | Biochem. Biophys. Res. Commun. 272:576-582(2000). | | | |
| SEQUENCE FROM N.A. | | | | | |
| RC | | SPECIES-Human; TISSUE-Amygdala; Pouska A., Wellenreuther R., Mewes H.-W., Well B., Wiemann S.; Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases. | | | |
| RA | | Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases. | | | |
| RL | | Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases. | | | |
| SEQUENCE FROM N.A. | | | | | |
| RC | | SPECIES-Rat; SPRAIN-Sprague-Dawley; Kim H., Park S., Kang Y., Kim C., Jeon J.; Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases. | | | |
| RA | | Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases. | | | |
| RL | | Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases. | | | |
| FUNCTION | | ORPHAN RECEPTOR. | | | |
| TISSUE SPECIFICITY | | IN HUMAN HIGHLY EXPRESSED IN BRAIN AND TESTIS. LOWER LEVELS IN SMALL INTESTINE, PLACENTA AND SPLEEN. IN BRAIN REGIONS DETECTED IN ALL REGIONS TESTED, BUT SOMEWHAT LOWER LEVELS IN THE CORPUS CALLOSUM, MEDULLA AND SPINAL CORD. IN THE MOUSE EXCLUSIVELY EXPRESSED IN BRAIN. | | | |
| SIMILARITY | | BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. | | | |
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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF250237; AAF79956.1; -
 DR EMBL: AB040800; BAA96646.1; -
 DR EMBL: AL161959; CAB82307.1; -
 DR EMBL: AF254416; AAF79959.1; -
 DR EMBL: AB040803; BAA96649.1; -
 DR EMBL: AF203907; AAC42284.1; -
 DR MIM: 605188; -
 DR MIM: MGI:1927851; GPR85; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 2.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECIP_F1_1; FALSE_NEG.
 DR PROSITE: PS0262; G-PROTEIN_RECIP_F2_1; -
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family.
 FT DOMAIN 1 25
 FT TRANSMEM 26 46 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 47 57 1 (POTENTIAL).
 FT TRANSMEM 58 78 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 79 96 2 (POTENTIAL).
 FT TRANSMEM 97 117 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 118 137 3 (POTENTIAL).
 FT TRANSMEM 138 158 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 159 188 4 (POTENTIAL).
 FT TRANSMEM 189 209 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 210 286 5 (POTENTIAL).
 FT TRANSMEM 287 307 6 (POTENTIAL).
 FT DOMAIN 308 313 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 314 334 7 (POTENTIAL).
 FT DOMAIN 335 370 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 94 172 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 370 AA; 41994 MW; 7B67A39F6166AEB CRC64;

Query Match 100.0%; Score 1963; DB 1; Length 370;
 Best Local Similarity 100.0%; Pred. No. 3e-126;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1. MANYSHADNILONSPFLATLKTSLGFTIGSVYVGNLISILVKKDTHRAVYFL 60
 DB 1 MANYSHADNILONSPFLATLKTSLGFTIGSVYVGNLISILVKKDTHRAVYFL 60
 61 DLCCSDILRSALICPEVFNYSVKNSTWYTGTLCKVIAFLGVLSCFHTAFMLFCISVTRY 120
 DB 61 DLCCSDILRSALICPEVFNYSVKNSTWYTGTLCKVIAFLGVLSCFHTAFMLFCISVTRY 120
 121 LATAHHEFYKRLFEWFCVAVICVWVTLVAMAPPVLDVGTYSIRREDOCTFHRSEFR 180
 DB 121 LATAHHEFYKRLFEWFCVAVICVWVTLVAMAPPVLDVGTYSIRREDOCTFHRSEFR 180
 121 LATAHHEFYKRLFEWFCVAVICVWVTLVAMAPPVLDVGTYSIRREDOCTFHRSEFR 180
 DB 121 LATAHHEFYKRLFEWFCVAVICVWVTLVAMAPPVLDVGTYSIRREDOCTFHRSEFR 180
 181 ANSLGEMLLATLLATLQVLYKLIFVHDKRKKRPQVFAAASQNTTFPGASGQAA 240
 DB 181 ANSLGEMLLATLLATLQVLYKLIFVHDKRKKRPQVFAAASQNTTFPGASGQAA 240
 241 ANSLGEMLLATLLATLQVLYKLIFVHDKRKKRPQVFAAASQNTTFPGASGQAA 240
 DB 241 ANSLGEMLLATLLATLQVLYKLIFVHDKRKKRPQVFAAASQNTTFPGASGQAA 240
 241 ANSLGEMLLATLLATLQVLYKLIFVHDKRKKRPQVFAAASQNTTFPGASGQAA 240
 DB 241 ANSLGEMLLATLLATLQVLYKLIFVHDKRKKRPQVFAAASQNTTFPGASGQAA 240
 301 YIVACYRVARAGVVGGLTAAVMSFAQAGINPFYCISNRLRRCSTTLTLCYCKS 360
 DB 301 YIVACYRVARAGVVGGLTAAVMSFAQAGINPFYCISNRLRRCSTTLTLCYCKS 360
 361 RLREPRYCVI 370
 DB 361 RLREPRYCVI 370

RESULT 2
 ID GP85_BRARE STANDARD: PRT: 371 AA.
 AC 091919;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Super conserved receptor expressed in brain 2.
 GN SREB2.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20294882; PubMed-10833454;
 RA Matsunoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
 RA Kobayashi M., Tadokoro M., Matsunoto S., Ohishi T., Furuchi K.;
 RT "An evolutionarily conserved G-protein coupled receptor family, SREB,
 RL expressed in the central nervous system."
 RL Biochem. Biophys. Res. Commun. 272:576-582(2000).
 CC -1- FUNCTION: ORPHAN RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS..

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 or send an email to license@isb-sib.ch).

DR EMBL: AB040805; BAA96651.1; -
 DR ZFIN: ZDB-GENE-000710-2; sreb2.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 2.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECIP_F1_1; FALSE_NEG.
 DR PROSITE: PS0262; G-PROTEIN_RECIP_F2_1; -
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family.
 FT DOMAIN 1 26
 FT TRANSMEM 27 47 1 (POTENTIAL).
 FT DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 79 2 (POTENTIAL).
 FT DOMAIN 80 96 3 (POTENTIAL).
 FT TRANSMEM 97 117 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 118 138 4 (POTENTIAL).
 FT TRANSMEM 139 159 5 (POTENTIAL).
 FT DOMAIN 160 189 6 (POTENTIAL).
 FT TRANSMEM 190 210 7 (POTENTIAL).
 FT DOMAIN 211 287 8 (POTENTIAL).
 FT TRANSMEM 288 308 9 (POTENTIAL).
 FT DOMAIN 309 321 10 (POTENTIAL).
 FT TRANSMEM 322 342 11 (POTENTIAL).
 FT DOMAIN 343 371 12 (POTENTIAL).
 FT DISULFID 95 173 BY SIMILARITY.
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 371 AA; 41954 MW; F6B6175BD3A348C2 CRC64;

Query Match 95.0%; Score 1865.5; DB 1; Length 371;
 Best Local Similarity 93.8%; Pred. No. 1.2e-119;
 Matches 348; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

1. MANYSHADNILONSPFLATLKTSLGFTIGSVYVGNLISILVKKDTHRAVYFL 59
 DB 1 MANYSHADNILONSPFLATLKTSLGFTIGSVYVGNLISILVKKDTHRAVYFL 60

| Query Match | Best Local Similarity | Score | DB 1 | Length | 387 |
|-------------|-----------------------|--------|------------------------------------|----------|------------|
| Matches 233 | Conservative | 62 | Mismatches 59 | Indels 3 | Gaps 22 |
| DOMAIN | 109 | 111 | EXTRACELLULAR (POTENTIAL) | | |
| FT | TRANSMEM | 132 | 3 (POTENTIAL) | | |
| FT | DOMAIN | 133 | CYTOPLASMIC (POTENTIAL) | | |
| FT | TRANSMEM | 154 | 4 (POTENTIAL) | | |
| FT | DOMAIN | 175 | EXTRACELLULAR (POTENTIAL) | | |
| FT | TRANSMEM | 203 | 5 (POTENTIAL) | | |
| FT | DOMAIN | 224 | CYTOPLASMIC (POTENTIAL) | | |
| FT | TRANSMEM | 302 | 6 (POTENTIAL) | | |
| FT | DOMAIN | 323 | EXTRACELLULAR (POTENTIAL) | | |
| FT | TRANSMEM | 336 | 7 (POTENTIAL) | | |
| FT | DOMAIN | 357 | CYTOPLASMIC (POTENTIAL) | | |
| FT | DISULFID | 110 | BY SIMILARITY | | |
| FT | CARBOHYD | 5 | N-LINKED (GLCNAC. . .) (POTENTIAL) | | |
| FT | CARBOHYD | 198 | N-LINKED (GLCNAC. . .) (POTENTIAL) | | |
| SEQ | SEQUENCE | 387 AA | 58094EFD4120871 CRC64 | | |
| Query Match | Best Local Similarity | 68.2% | Score 1339.5 | DB 1 | Length 387 |
| Matches 233 | Conservative | 62 | Mismatches 59 | Indels 3 | Gaps 22 |
| DOMAIN | 109 | 111 | EXTRACELLULAR (POTENTIAL) | | |
| FT | TRANSMEM | 132 | 3 (POTENTIAL) | | |
| FT | DOMAIN | 133 | CYTOPLASMIC (POTENTIAL) | | |
| FT | TRANSMEM | 154 | 4 (POTENTIAL) | | |
| FT | DOMAIN | 175 | EXTRACELLULAR (POTENTIAL) | | |
| FT | TRANSMEM | 203 | 5 (POTENTIAL) | | |
| FT | DOMAIN | 224 | CYTOPLASMIC (POTENTIAL) | | |
| FT | TRANSMEM | 302 | 6 (POTENTIAL) | | |
| FT | DOMAIN | 323 | EXTRACELLULAR (POTENTIAL) | | |
| FT | TRANSMEM | 336 | 7 (POTENTIAL) | | |
| FT | DOMAIN | 357 | CYTOPLASMIC (POTENTIAL) | | |
| FT | DISULFID | 110 | BY SIMILARITY | | |
| FT | CARBOHYD | 5 | N-LINKED (GLCNAC. . .) (POTENTIAL) | | |
| FT | CARBOHYD | 198 | N-LINKED (GLCNAC. . .) (POTENTIAL) | | |
| SEQ | SEQUENCE | 387 AA | 58094EFD4120871 CRC64 | | |

CORTEX.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL: AB040801; BAA96647.1; -
 DR MIM: 300253; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.

FT DOMAIN 1 26
 FT TRANSMEM 27 47
 FT DOMAIN 48 59
 FT TRANSMEM 60 80
 FT DOMAIN 81 97
 FT TRANSMEM 98 118
 FT DOMAIN 119 139
 FT TRANSMEM 140 160
 FT DOMAIN 161 188
 FT TRANSMEM 189 209
 FT DOMAIN 210 287
 FT TRANSMEM 288 308
 FT DOMAIN 309 322
 FT TRANSMEM 323 343
 FT DOMAIN 344 373
 FT DISULFID 96 174
 FT CARBOHYD 3 184
 FT CARBOHYD 184 184
 SO SEQUENCE 373 AA: 41481 MW: 8A227F914C9D8358 CRC64;

Query Match 65.4%; Score 1283.5; DB 1; Length 373;
 Best Local Similarity 62.3%; Pred. No. 2.7e-80;
 Matches 233; Conservative 56; Mismatches 80; Indels 5; Gaps 3;

QY 1 MANYSHADNIIONLS--LTAFILKLTSLGFIIGSVGNLISILVCKTLHRAPIYF 58
 DB 1 MANTTGEPEVSGALSPSASAYKVLGLGIMCVSLAGNAISLVLKRALHAKAPIYF 60
 QY 59 LLDLCCSDILRSALCEPFVNSVKNSTWYGTLLCKVIAFLGVLSCEHTAFMLFCISVT 118
 DB 61 LLDLCLADIRSAVCEPFVLASVRHSSWTFMSCKIYAFMAVLCEFHAFMLFCISVT 120
 QY 119 RLALAHNHFYKRLFTWCLAVICWVTLISVAMAPPVLVDVTSYFIREDOCTQHR 178
 DB 121 RYMAALAHNHFYKRLMTLCAVTCAMVLSVAMAPPVFDVGTYSFIREDOCIENHR 180
 QY 179 FRANDSLGFMILLALILLTOLVYLKLFVHDKRKKPPOFAVAAVSOMTFHGPASGQ 238
 DB 181 FRANDTLGFMILLAVYMAATHAVYGLLFEYHRKMKKPYOMPAISOMTFHGPATIGQ 240
 QY 239 AAANMLAGRGPTPEPTLLGIRONANTTGRRLVLDEKEMKRISRMFYIMTFLELLTW 298
 DB 241 AAANMLAGRGPMPTLLGIRONGHAAS--RLTIGMDEVKGEQOLGRMFVAITLLLELLW 299
 QY 299 GYLVACYKRVARAGVYVGGFLTAAVMSFPAQGINPFYCISNRELRCFST--TLTY 336
 DB 300 SYIYACVYRVVAKCAVHYRLATAVMSFQAQAVNPYVCFLLNDLKKCLRTHAPCWG 359
 QY 357 CRKSLRPREPYCVI 370
 DB 360 TGGAPAPRPREPYCVI 373

RESULT 5

SRB3_RAT ID STANDARD: PRT; 373 AA.

AC 09JTH2;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Super conserved receptor expressed in brain 3.
 GN SREB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_Taxid=10116;
 RX MEDLINE=2029482; PubMed=10833454;
 RC TISSUE=Brain;
 RP SEQUENCE FROM N.A.

RA Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
 RA Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuchi K.,
 RT "An evolutionarily conserved G-protein coupled receptor family, SREB,
 RT expressed in the central nervous system."
 CC Blochem. Biophys. Res. Commun. 272:576-582(2000).
 CC -1- FUNCTION: ORPHAN RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL: AB040804; BAA96650.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.

FT DOMAIN 1 26
 FT TRANSMEM 27 47
 FT DOMAIN 48 59
 FT TRANSMEM 60 80
 FT DOMAIN 81 97
 FT TRANSMEM 98 118
 FT DOMAIN 119 139
 FT TRANSMEM 140 160
 FT DOMAIN 161 188
 FT TRANSMEM 189 209
 FT DOMAIN 210 287
 FT TRANSMEM 288 308
 FT DOMAIN 309 322
 FT TRANSMEM 323 343
 FT DOMAIN 344 373
 FT DISULFID 96 174
 FT CARBOHYD 3 184
 FT CARBOHYD 184 184
 SO SEQUENCE 373 AA: 41511 MW: C06DEA2F0E88CAFS CRC64;

Query Match 65.0%; Score 1276.5; DB 1; Length 373;
 Best Local Similarity 62.3%; Pred. No. 8.1e-80;
 Matches 233; Conservative 55; Mismatches 81; Indels 5; Gaps 3;

QY 1 MANYSHADNIIONLS--LTAFILKLTSLGFIIGSVGNLISILVCKTLHRAPIYF 58
 DB 1 MANTTGEPEVSGALSPSASAYKVLGLGIMCVSLAGNAISLVLKRALHAKAPIYF 60
 QY 59 LLDLCCSDILRSALCEPFVNSVKNSTWYGTLLCKVIAFLGVLSCEHTAFMLFCISVT 118

```

DB 61 LDDLCADGIRSAICPPVILASVHRSSWTFSLSCITVAFMAVLFCFHAFMLFCISVT 120
OY 119 RLTAIAHHRFYKRLTFWTCIAVICWMTLSVMAAPPPVLDVGTYSIFREDOCTEQHS 178
DB 121 RYMAIAHHRFYKRLTFWTCIAVICWMTLSVMAAPPPVLDVGTYSIFREDOCTEQHS 180
OY 179 FRANSISGEMLLALLLTLTOLVYLLTFVHRRKMKRPQFAAASQNTTFPGASGQ 238
DB 181 FRANDTLGEMLLAVALMAATHAVYGRLLTFEYHRRKMKRPQFAAASQNTTFPGASGQ 240
OY 239 AAANWLAGCGRPTPTLLGIRONANTTGRRLVLDDEFKMERKISMFTYIMFELTLM 298
DB 241 AAANWLAGCGRPTPTLLGIRONANTTGRRLVLDDEFKMERKISMFTYIMFELTLM 299
OY 299 GGLVACVYRVFARGPVYDGFLLTAAVWMSFAQAGINPVCIFSNRELRCFST- "TLLY 356
DB 300 SPYIACVYRVFARGPVYDGFLLTAAVWMSFAQAGINPVCIFSNRELRCFST- "TLLY 359
OY 357 CRKSLRPREPCYI 370
DB 360 TCGAPAPREPCYI 373

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RESULT 6
ID GPRS_HUMAN STANDARD: PRT: 375 AA.
AC Q9NS67;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G protein-coupled receptor GPR27 (Super conserved receptor
  expressed in brain 1).
GN GPR27 OR SREB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20294882; PubMed=10833454;
RA Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
  Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K.;
  "An evolutionarily conserved G-protein coupled receptor family, SREB,
  expressed in the central nervous system.";
  Biochem. Biophys. Res. Commun. 272:576-582(2000).
RL 1- FUNCTION: ORPHAN RECEPTOR. POSSIBLE CANDIDATE FOR AMINE-LIKE G-
  PROTEIN COUPLED RECEPTOR.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC 1- TISSUE SPECIFICITY: HIGHLY EXPRESSED AS A 3.0 KB TRANSCRIPT IN
  BRAIN, OVARY, TESTIS, HEART, PROSTATE AND PERIPHERAL LEUKOCYTES.
CC LOWER LEVELS IN PANCREAS AND SMALL INTESTINE. A 2.3 KB TRANSCRIPT
  WAS ALSO FOUND IN PERIPHERAL LEUKOCYTES. IN BRAIN REGIONS,
  DETECTED AS A 3.0 KB TRANSCRIPT IN ALL REGIONS TESTED. HIGHEST
  LEVELS IN THE CADATE NUCLEUS, PUTAMEN, HIPPOCAMPUS AND
  SUBTHALAMIC NUCLEUS. LOWEST LEVEL IN THE CEREBELLUM.
CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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  or send an email to: license@sib-sib.ch).
CC
CC EMBL, AB040799; BAA96645.1;
CC
CC MIM: 605187;
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm.1.1.
CC PRINTS: PR000237; GPCR_RHODOPSIN.
CC PROSITE, PS00237; G-PROTEIN_RECPT_FL_1; FALSE_NEG.

```

```

DR PROSITE: PS00262; G-PROTEIN_RECPT_FL_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 23
FT TRANSSEM 24 44
FT DOMAIN 45 55
FT TRANSSEM 56 76
FT DOMAIN 77 97
FT TRANSSEM 98 118
FT DOMAIN 119 139
FT TRANSSEM 140 160
FT DOMAIN 161 181
FT TRANSSEM 182 202
FT DOMAIN 203 285
FT TRANSSEM 286 306
FT DOMAIN 307 320
FT TRANSSEM 321 341
FT DOMAIN 342 375
FT DISULFID 95 171
FT CARBOHYD 3
SQ SEQUENCE 375 AA; 39818 MW; E17AF3D86FD47204 CRC64;

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Query Match 50.9%; Score 998.5; DB 1; Length 375;
 Best Local Similarity 55.2%; Pred. No. 5.2e-61;
 Matches 190; Conservative 51; Mismatches 96; Indels 7; Gaps 3;

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OY 22 LKLTSLGFIIGSVVGNLISILVKKDKTLRARAYFLLDCCSDILSAICPPFVNSV 81
DB 20 LKLTSLGFIIGSVVGNLISILVKKDKTLRARAYFLLDCCSDILSAICPPFVNSV 79
OY 82 KNSGTWT--YGLTCKVIAFLGVLSCFHAFMLFCISVTRYIAIAHHRFYKRLTFWTC 138
DB 80 RRAAAGAPPGALGCKLAFALFCFHAFMLFCISVTRYIAIAHHRFYKRLTFWTC 139
OY 139 LA-VICWMTLSVMAAPPPVLDVGTYSIFREDOCTEQHSFRANDSISGEMLLALLILA 197
DB 140 AAMLVCAAMALALAAAPPPVLDVGTYSIFREDOCTEQHSFRANDSISGEMLLALLILA 196
OY 198 TOLVYLKIFVHRRKMKRPQFAAASQNTTFPGASGQAAANWLAGCGRPTPTLL 257
DB 197 TOLVYLKIFVHRRKMKRPQFAAASQNTTFPGASGQAAANWLAGCGRPTPTLL 256
OY 258 GIRONANTTGRRLVLDDEFKMERKISMFTYIMFELTLMGPYLVACVYRVFARGPV 317
DB 257 GIRPAGGRARRLVLDDEFKMERKISMFTYIMFELTLMGPYLVACVYRVFARGPV 316
OY 318 GGLTAAVWMSFAQAGINPVCIFSNRELRCFSTTLLYCRKR 361
DB 317 QAVLTASVWLTFAQAGINPVCIFSNRELRCFSTTLLYCRKR 360
RESULT 7
ID GPRS_RAT STANDARD: PRT: 377 AA.
AC Q9JUH3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G protein-coupled receptor GPR27 (Super conserved receptor
  expressed in brain 1).
GN GPR27 OR SREB1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20294882; PubMed=10833454;
RA Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
  Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K.;
  "An evolutionarily conserved G-protein coupled receptor family, SREB,

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Best Local Similarity 55.1%; Pred. No. 2,3e-60;
Matches 188; Conservative 51; Mismatches 96; Indels 6; Gaps 3

OY 22 LKLTSLGFIIVGVNGLISILVYKDKTLHRAPIYELDLCCSDILRSALCEPFVNSV 81
D 23 LRLATLSLLCVSLAGNVLFALILVERSLHRAPIYLLDLCLADLRADLACIPAVMLAA 82
OY 82 KNGSF--WTYGLTCKVIAFLGVLSCFTAFELFCISTRIYAIHHHRYTKRLTFWTC 138
D 83 RRAAAAAGTPPALCGCKTLIAFLAALFCFFAAAFLLLCVGYTRYLAIAHHHREYERLAWGPC 142
OY 139 LA-VICMWTLISVAMAFPPYLDVGTSTFIREDOQCFHRSFRANDSLFEMLLAILLA 197
D 143 AAMLYCAAMALMLAAAFPPYLDGGAD--DEDAPCALERPDPGAPGALFLLLAAVGA 200
OY 198 TOLVYLKLTLEFVHRRKMKPVQVAVASONTFFHGGAGAGAAANLAGEGRPTPTLL 257
D 201 THLYVLRILFLFIDRRKMRPARLVPAVSHDMTFHGARGAGAAANTAFGRGPTPTPALY 260
OY 258 GIRQANANTTGRRLVLVDEFFKMEKRISRMFYIMTFLFLTLMGPIVACYRWFAFGPV 317
D 261 GIRPAGPGRGARRLLVLEEFKTEKRIKCFKMFYITLLFLMLMGPYVAVSLRYLVRGAVP 320
OY 318 GGFLLAAVWMSFAQGINPFVCIFSRRELRKRFSTLLXCR 358
D 321 QAVLTASVWLTFQAQINPVGFLNRELRLDQFRAQFPCCQ 361

RESULT 9
CCKR_XENLA STANDARD: PRT: 453 AA.
ID CCKR_XENLA STANDARD: PRT: 453 AA.
AC P70031.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cholecystokinin receptor (CCK-XLR).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96319796; PubMed=8700154;
RA Schmitz F., Pratt D.S., Wu M.-J., Kolakowski L.F. Jr., Beilborn M.,
RA Kopin A.S.;
RT "Identification of cholecystokinin-B/gastrin receptor domains that
RT confer high gastrin affinity: utilization of a novel xenopus laevis
RT cholecystokinin receptor.";
RL Mol. Pharmacol. 50:436-441(1996).
CC -!- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. THIS RECEPTOR MEDIATES ITS
CC ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. HAS HIGH
CC AFFINITY FOR CCK-8 AND LOW AFFINITIES FOR GASTRIN-17-1, CCK-4, AND
CC UNSULFATED CCK-8.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN AND STOMACH.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HAS EQUAL SIMILARITY TO TYPE A AND B CHOLECYSTOKININ MAMMALIAN
CC RECEPTORS.
CC
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CC
CC EMBL, U09258; AAB09052.1; -.
CC GCRDB: GCR_0930; -.
CC GCRDB: GCR_1953; -.

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| | | |
|----|----------------------------------------------------------------------------------|------------------------------------------|
| DR | InterPro: IPR000276; GPCR_Rhodpsn. | |
| DR | Pfam: PF00001; 7tm_1; 1. | |
| DR | PRINTS: PR00237; GPCR_RHODOPSIN. | |
| DR | PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1. | |
| DR | PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1. | |
| KW | G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate. | |
| FT | DOMAIN | 1 64 |
| FT | TRANSMEM | 65 94 |
| FT | DOMAIN | 95 104 |
| FT | TRANSMEM | 105 131 |
| FT | DOMAIN | 132 142 |
| FT | TRANSMEM | 143 164 |
| FT | DOMAIN | 165 184 |
| FT | TRANSMEM | 185 205 |
| FT | DOMAIN | 206 237 |
| FT | TRANSMEM | 238 261 |
| FT | DOMAIN | 262 343 |
| FT | TRANSMEM | 344 364 |
| FT | DOMAIN | 365 379 |
| FT | TRANSMEM | 380 403 |
| FT | DOMAIN | 404 453 |
| FT | DISULFID | 141 223 |
| FT | LIPID | 401 401 |
| FT | CARBOHYD | 9 9 |
| FT | CARBOHYD | 22 22 |
| FT | CARBOHYD | 30 30 |
| FT | CARBOHYD | 35 35 |
| FT | CARBOHYD | 39 39 |
| FT | SEQUENCE | 453 AA; 51157 MW; 062192787482678 CRC64; |

| Query Match | 13.1% | Score 257.5 | DB 1 | Length 453 |
|-----------------------|------------------------------------------|--------------------------------------------------------------|-----------|------------|
| Best Local Similarity | 24.2% | Pred. No. 7.9e-11 | | |
| Matches 92 | Conservative 65 | Mismatches 164 | Indels 59 | Gaps 11 |
| QY | 16 | SPLEAFILSLIGFLIGSVVGNLLISILVYKDKTLHRAPYFFLLDCCSDILRSALICFP | 75 | |
| DB | 64 | SDLNLMVRIWVSVYFELLSVFGNTLIIIVLVNKKRLRITTFNSFLSLASLDLMAVLICMP | 123 | |
| QY | 76 | FVF--NSAKNGSTWYTGILTCKVIAFLVGLSCFHFAFMFLCISVTRYLAIAH--HREYT | 130 | |
| DB | 124 | FTLLPNLMEN--FIEGVCICRAAAYFMGLSVSTFNLVAISIRYSALICNPILKSRWQ | 180 | |
| QY | 131 | KRLPFTCLAVICWMTLSVAMAFPPVLDVGYSTRREE---DQCTQHSFRANDISG | 186 | |
| DB | 181 | TRSHAY---RVIAATWVLSSTIMTDLYLVNKTIVTFPMKDRRYGHCRCLPMPKQYQQA-W | 236 | |
| QY | 187 | FMLLATALLATOLVYLKLIFFVHDDRKKKPPQFPAASQMTFHPGSGAGGAANWLAG | 246 | |
| DB | 237 | YVLLITLITLIFIPGVMI-VAGGLISRELRYRGQFMDLKKKKAIRKNGV----- | 285 | |
| QY | 247 | FGGCTPPTL-----LGIRONANTTGGRRLLVLDEFKME-----KR | 282 | |
| DB | 286 | -----TPTTIPSGDGDGDCYIQVTKRRNTMEMSTLTPSVCTKMDRARINNSEAKIMAKKR | 340 | |
| QY | 283 | ISRMFYMTFLFLFLMGVYLACVWRV---ARGVYVGGFLTAVMMSFPAQAGINPEVC | 339 | |
| DB | 341 | VIRMLIVVAFFICOMBIYVANTWAKADELSAENFTLIGAPISFTILLSTYSACVNPITY | 400 | |
| QY | 340 | IFSNEIRLRCFSTLLYCRK | 359 | |
| DB | 401 | CFMKNRFRKAFLGTFSSCIC | 420 | |
| RESULT | 10 | | | |
| ID | GREL_BALAM | STANDARD | PRT | 476 AA. |
| AC | 093126 | 093128 | | |
| DT | 30-MAY-2000 | (Rel. 39, Last sequence update) | | |
| DT | 30-MAY-2000 | (Rel. 39, Last sequence update) | | |
| DT | 16-OCT-2001 | (Rel. 40, Last annotation update) | | |
| DE | Probable G protein-coupled receptor NO9. | | | |

OS Balanus amphitrite (Barnacle).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Cirripedia;
OC Thoracica; Sessilia; Balanomorpha; Balanoidae; Balanidae; Balanus.
OX NCBI_TaxID=32267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DARWIN;
RX MEDLINE=97074655; PubMed=8917082;
RA Isotal A., Kawahara H., Okazaki Y., Shizuri Y.;
RT "Molecular cloning of a new member of the putative G protein-coupled
RT receptor gene from barnacle Balanus amphitrite.";
RL Gene 175:95-100(1996)
CC - FUNCTION: ORPHAN G-PROTEIN COUPLED RECEPTOR.
CC - SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC MOST SIMILAR TO ALPHA-2-ADRENERGIC RECEPTORS.
CC -----
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DR EMBL: D78363; BA11375.1;
DR EMBL: D78587; BA11424.1;
DR GCRDB: GCR_1153;
DR GCRDB: GCR_1154;
DR Interpro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 36
FT TRANSSEM 37 60 1 (POTENTIAL).
FT DOMAIN 61 69 1 (POTENTIAL).
FT TRANSSEM 70 93 2 (POTENTIAL).
FT DOMAIN 94 103 3 (POTENTIAL).
FT TRANSSEM 104 127 3 (POTENTIAL).
FT DOMAIN 128 152 4 (POTENTIAL).
FT TRANSSEM 153 172 4 (POTENTIAL).
FT DOMAIN 173 200 5 (POTENTIAL).
FT TRANSSEM 201 221 5 (POTENTIAL).
FT DOMAIN 222 375 6 (POTENTIAL).
FT TRANSSEM 376 396 6 (POTENTIAL).
FT DOMAIN 397 406 7 (POTENTIAL).
FT TRANSSEM 407 430 7 (POTENTIAL).
FT DOMAIN 431 476 7 (POTENTIAL).
FT SITE 113 113
FT SITE 208 208
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 192 BY SIMILARITY.
FT CONFLICT 454 454 R -> A (IN REF. 1; BA11424).
SO SEQUENCE 476 AA; 53245 MW; 0F55B51595D5CD06 CRC64;

Query Match 13.18; Score 257.5; DB 1; Length 476;
Best Local Similarity 21.68; Pred. No. 8.2e-11;
Matches 101; Conservative 60; Mismatches 173; Indels 133; Gaps 15;

QY 8 ADNLIONLS---PLTAF-----LKLTSIGFIISVSVGNLISILVKKTKLRAPRY 57
DB 11 ADVNTLVNSGRPATLFWADHRLISLALFLNLVVAAGNLVMAVAVFSKLPVTNL 70
QY 58 FLIDLCSSDIRSAICPEFVNSVNGSTWYGTLCVIAFLVGLSCFHTAFMLFCISV 117
DB 71 FIVSLACADLVGMVLVLPF-SATLEVLVDWVLXGDVWCWVLAVDVMCTSLINCAISL 129

QY 118 TRYLAIAHREYTKRLTEFWTCLAVICWYTLNVMAFPVLD----VGYTSFIREDQCT 173
DB 130 DRYLVASOPISYPSMSTRANOKLAAVWVLSFICFPPLVGMNDPRGTILSGSSACR 189
QY 174 F-----QHRSFANDSLGEMLLALILATOLVYLKLFVHDDRKKMKVQVFAAVSQMW 228
DB 190 LTCELTENERGYIYASLGSFLLPSTYML-----FFYGRIRYTRAVSTTRALAQGF 238
QY 229 -----TFHGPASGOAAMNLA-- 245
DB 239 RTTKDEEGRLTLRIHGRSVYTORAEQAAAGARAHGOVRLTISEGARKONKPSFVHC 298
QY 246 -----GGR-----GPTPTLIG---IRON 262
DB 299 REDSRAKNQYEITYYVEGSGRGRVPOPOPRAKLISASQSEDDSRPPRTISRVSRRR 358
QY 263 ANTGRRRLVLDEFEMERISRMFYIMFLFLTMGLPVLVACWYVFRG---PVPVPG 319
DB 359 VHQARR-----FRMEKRAKTVGIYGLFILCHLPFFV-CY---LYRGFADCVPL 407
QY 320 FLTAAVWMSFAQGINPEVCIFSNRELRCFSTTL--LYCRSRRLPR 364
DB 408 LFSVFELGLYCSAVVPCVYALCSRDREAFSSILCKCYCRGRAMER 454

RESULT 11
5H2A_HUMAN STANDARD: PRT: 471 AA.
ID 5H2A_HUMAN
AC P28223;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-Hydroxytryptamine 2A receptor (5-HT-2A) (Serotonin receptor)
DE (5-HT-2)
GN HTR2A OR HTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=92109767; PubMed=1722404;
RA Saltzman A.G., Morse B., Whitman M.M., Ivanschchenko Y., Jaye M.,
RA Felder S.;
RT "Cloning of the human serotonin 5-HT2 and 5-HT1C receptor subtypes.";
RL Biochem. Biophys. Res. Commun. 181:1469-1478(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92356792; PubMed=1323014;
RA Chen K., Yang W., Grimsby J., Shih J.C.;
RT "The human 5-HT2 receptor is encoded by a multiple intron-exon gene.";
RL Brain Res. Mol. Brain Res. 14:20-26(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94308772; PubMed=8035173;
RA Cook E.H. Jr., Fletcher K.E., Walnwright M., Marks N., Yan S.Y.,
RA Leventhal B.L.;
RT "Primary structure of the human platelet serotonin 5-HT2A receptor:
RT identify with frontal cortex serotonin 5-HT2A receptor.";
RL J. Neurochem. 63:465-469(1994).
RN [4]
RP SEQUENCE OF 9-464 FROM N.A.
RC TISSUE=Brain;
RA Tritsch R.J., Robinson D.L., Sahagan B.G., Horlick R.A.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 105-218 FROM N.A.
RX MEDLINE=93049882; PubMed=1330647;
RA Stam N.J., van Huizen F., van Alebeek C., Brands J., Dijkema R.,
RA Tonnaer J.A., Olijve W.;
RT "Genomic organization, coding sequence and functional expression of
RT human 5-HT2 and 5-HT1A receptor genes.";

| FT | DISLFTD | 148 | 227 | BY | SIMILARITY. |
|----|----------|---------|-----------|-------------------|-------------|
| FT | VARIANT | 25 | 25 | T -> N. | |
| FT | VARIANT | 452 | 452 | /FTID-VAR_003448. | |
| FT | | | | H -> Y. | |
| FT | | | | /FTID-VAR_003449. | |
| SO | SEQUENCE | 471 AA; | 52603 MM; | EFBAAC0BC5379DA2 | CRC64; |

| Query Match | 12.9%; | Score 253.5; | DB 1; | Length 471; |
|-----------------------|------------------|--------------------|------------|-------------|
| Best Local Similarity | 24.8%; | Pred. No. 1.5e-10; | | |
| Matches 84; | Conservative 61; | Mismatches 147; | Indels 47; | Gaps 11 |

| OY | 30 | IIGVGVGNMLISILVADKTYLRAPRYFLDLCSSDIIRSAICPEFVSNKSGSTWY | 89 |
|---------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------|-----|
| DB <td>84</td> <td>VILITAGNIIIVIMAVSEIKLQNTANTYFMISLAIDMLGLFVMPVSMITLYGYRMP</td> <td>143</td> | 84 | VILITAGNIIIVIMAVSEIKLQNTANTYFMISLAIDMLGLFVMPVSMITLYGYRMP | 143 |
| OY <td>90</td> <td>GLTCKVIAFLGVLSCFHTAFMLFCISVRYLAIA----HHFFYTKRLTFWCLANTCY</td> <td>145</td> | 90 | GLTCKVIAFLGVLSCFHTAFMLFCISVRYLAIA----HHFFYTKRLTFWCLANTCY | 145 |
| DB <td>144</td> <td>PSKLCAMVITLDVLTSTASIMHLCAISIDRYAIAQNPIHHSRNSRTKAFKIIA----</td> <td>199</td> | 144 | PSKLCAMVITLDVLTSTASIMHLCAISIDRYAIAQNPIHHSRNSRTKAFKIIA---- | 199 |
| OY <td>146</td> <td>WLSVIAAF--PVLGVGYVSFIREDOCFQHRSPFANDSLCFEMLLAILATOLVYLK</td> <td>204</td> | 146 | WLSVIAAF--PVLGVGYVSFIREDOCFQHRSPFANDSLCFEMLLAILATOLVYLK | 204 |
| DB <td>200</td> <td>WTISGISNPRIPEVLQDDSKYFKEGSCLL-----ADDN--FVLGGSVSPFIPLTIV</td> <td>251</td> | 200 | WTISGISNPRIPEVLQDDSKYFKEGSCLL-----ADDN--FVLGGSVSPFIPLTIV | 251 |
| OY <td>205</td> <td>LIFVHDKRMKRVQVFVAVSONMTFHPGASGOAANMLAGFGNGPTPTLGI-----</td> <td>259</td> | 205 | LIFVHDKRMKRVQVFVAVSONMTFHPGASGOAANMLAGFGNGPTPTLGI----- | 259 |
| DB <td>252</td> <td>ITYFL-----TISLQKEATLC-----VSDLGTRAKLASFSF--LPQSSISSEKLFQ</td> <td>296</td> | 252 | ITYFL-----TISLQKEATLC-----VSDLGTRAKLASFSF--LPQSSISSEKLFQ | 296 |
| OY <td>260</td> <td>----RQNTANTYGRRLVLVDEFKMERKISRMYIMTFELTLMGPYLVACYRVPAR---</td> <td>312</td> | 260 | ----RQNTANTYGRRLVLVDEFKMERKISRMYIMTFELTLMGPYLVACYRVPAR--- | 312 |
| DB <td>297</td> <td>RSIHREPSGYTGR---TMOISINQCKACKVIGIYFELFVVMGCFEITINIMAVICKESC</td> <td>353</td> | 297 | RSIHREPSGYTGR---TMOISINQCKACKVIGIYFELFVVMGCFEITINIMAVICKESC | 353 |
| OY <td>313</td> <td>GPVVPGEFLTAAVMSFPAQAGINPVCIFSNELRCPS</td> <td>351</td> | 313 | GPVVPGEFLTAAVMSFPAQAGINPVCIFSNELRCPS | 351 |
| DB <td>354</td> <td>NEDVIGALLNFWMIGLSSAVNPVLTLEMTYSAES</td> <td>392</td> | 354 | NEDVIGALLNFWMIGLSSAVNPVLTLEMTYSAES | 392 |

| SH2A_MACMU | STANDARD: | PRT: | 471 AA. |
|------------|---------------------------------------------------------------------|------|---------|
| DT | 01-0CT-1996 (Rel. 34, Created) | | |
| DT | 01-0CT-1996 (Rel. 34, Last sequence update) | | |
| DT | 01-0CT-1996 (Rel. 34, Last annotation update) | | |
| DE | 5-hydroxytryptamine 2A receptor (5-HT-2A) (Serotonin receptor) | | |
| DE | (5-HT-2). | | |
| GN | HT2A. | | |
| OS | Macaca mulatta (Rhesus macaque). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; | | |
| OC | Cercopithecoidea; Macaca. | | |
| OX | NCBI_TaxID=9544; | | |
| RN | [1] | | |
| RA | SEQUENCE FROM N.A. | | |
| RA | MEDLINE=95315240; PubMed=7794950; | | |
| RA | Johnson M.P., Baez M., Kursar J.D., Nelson D.L.; | | |
| RT | "Species differences in 5-HT2A receptors: cloned pig and rhesus | | |
| RT | monkey 5-HT2A receptors reveal conserved transmembrane homology to | | |
| RT | the human rather than rat sequence." | | |
| RL | Biochim. Biophys. Acta 1236:201-206(1995). | | |
| CC | -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR | | |
| CC | 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS | | |
| CC | AS A NEUROTANSITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR | | |
| CC | MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE | | |
| CC | A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS | | |
| CC | RECEPTOR IS INVOLVED IN TRACHEAL SMOOTH MUSCLE CONTRACTION, | | |
| CC | BRONCHOCONSTRICITION, AND CONTROL OF ALDOSTERONE PRODUCTION. | | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein. | | |
| CC | -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. | | |
| CC | STRONGEST TO THE OTHER 5HT-2 SUBTYPE RECEPTORS. | | |

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| | Matches | 86; | Conservative | 67; | Mismatches | 150; | Indels | 50; | Gaps | 13; |
|----|---------|-----------------------------------------------------------------|--------------|-----|------------|------|--------|-----|------|-----|
| QY | 30 | IIGVGVGNGLISILLVYDKTLHAPRYFLDLCCSDIIRASICEPEFVNSVKNSTWY | 89 | | | | | | | |
| | | : | | | | | | | | |
| Db | 84 | VILITACNIIITIVAMVSEKTLQNTATNFVLMSLAIADMLGLVMPVSMILITLYGRMPL | 143 | | | | | | | |
| | | : | | | | | | | | |
| QY | 90 | GLTCKVIAFLGVLSCFHTAFMLFCISTRYLAIA----HHFFYKRLTFMTCLAVICMY | 145 | | | | | | | |
| | | : | | | | | | | | |
| Db | 144 | PSKLCIAVVIYLDVLESTASIMHLCAISLDRYVAIONPPIHSHFSNSTRKFLKIIA---V | 199 | | | | | | | |
| | | : | | | | | | | | |
| QY | 146 | WTLSSVAAFP--FVLDVGYGVTSFIREDOCTQFQRSPRANSIDLGFMILLILATOLVYK | 204 | | | | | | | |
| | | : | | | | | | | | |
| Db | 200 | WTISGVGMPPIPVBELODDSKYFKGSGCL-----ADDN--FVLIGSVAFPIITIMV | 251 | | | | | | | |
| | | : | | | | | | | | |
| QY | 205 | LIFVYHDRKKMKPVQFVAAVSONMTFHHGPGASGQAANMLAGFGGPPPTPLGI----- | 259 | | | | | | | |
| | | : | | | | | | | | |
| Db | 252 | ITYFL-----TIKSLQKEATLC-----VSDLESTRAKLASFSF--LPQSLSEBKLFQ | 296 | | | | | | | |
| | | : | | | | | | | | |
| QY | 260 | ---RQANANTGRRRLVLVDEFKMKRISRMEFYIMTFLEFLTIMGPYLVACYRWVFAR--- | 312 | | | | | | | |
| | | : | | | | | | | | |
| Db | 297 | RSIHREPSSTYGR---TMOISINBOKACKAKVLGIYFFLEFVVMWCEPFETINIMAVICKESC | 353 | | | | | | | |
| | | : | | | | | | | | |
| QY | 313 | GPVYVGGFLTAAVMMSFAQAGINPVCIFSNELRCESTILLVC--KSRILP | 363 | | | | | | | |
| | | : | | | | | | | | |
| Db | 354 | NEHYIGALLANFVWIGLSSAVNPVYLLFNKTYSAFS--RYIQOQYENRRP | 405 | | | | | | | |
| | | : | | | | | | | | |

| | | | | |
|------------|--------------------------------------------------------------------------------------------------------------------------|-----------------------------------|------|----------------------------|
| | RESULT | 14 | | |
| OPN3_MOUSE | OPN3_MOUSE | STANDARD; | PRT: | 400 AA. |
| AC | Q9WUR7 | | | |
| DT | 16-OCT-2001 | (Rel. 40, Created) | | |
| DT | 16-OCT-2001 | (Rel. 40, Last sequence update) | | |
| DE | 16-OCT-2001 | (Rel. 40, Last annotation update) | | |
| DE | Opsin 3 (Encephalopsin) (Panopsin). | | | |
| GN | OPN3 OR BCPN. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| CC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCB1_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=99252448; PubMed=10234000; | | | |
| RA | Blackshaw S., Snyder S.H.; | | | |
| RT | "encephalopsin: a novel mammalian extraretinal opsin discretely | | | |
| RL | localized in the brain."; | | | |
| J. | Neurosci. 19:3681-3690(1999). | | | |
| - | FUNCTION: May play a role in encephalic photoreception. | | | |
| - | SUBCELLULAR LOCATION: Integral membrane protein. | | | |
| - | SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. | | | |
| CC | OPSIN SUBFAMILY. | | | |
| CC | | | | |
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| CC | modified and this statement is not removed. Usage by and for commercial | | | |
| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | |
| CC | or send an email to license@isb-sib.ch). | | | |
| EMBL | AFL140241; AAD32670.1; . | | | |
| DR | MGD; MG1:1338022; Opn3. | | | |
| DR | InterPro; IPR000276; GPCR_Rhodopsn. | | | |
| DR | Pfam; PF00001; 7tm_1; 1. | | | |
| DR | PRINTS; PF00237; GPCRRHODOPSN. | | | |
| DR | PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1. | | | |
| DR | PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. | | | |
| DR | PROSITE; PS00238; Opsin; 1. | | | |
| KW | Photoreceptor; Retinal protein; Transmembrane; Lipoprotein; Palmitate; | | | |
| KM | G-protein coupled receptor. | | | |
| FT | DOMAIN | 1 | 38 | EXTRACELLULAR (POTENTIAL); |
| FT | TRANSMEM | 39 | 63 | 1 (POTENTIAL). |
| FT | DOMAIN | 64 | 75 | CYTOPLASMIC (POTENTIAL); |

| FT | TRANSMEM | 76 | 100 | 2 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
|-----|----------|---------|-----------|-----------------|----------------------------|
| FT | DOMAIN | 101 | 115 | 3 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 116 | 135 | 4 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| FT | DOMAIN | 136 | 151 | 5 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 152 | 175 | 6 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| FT | DOMAIN | 176 | 199 | 7 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 200 | 227 | 8 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| FT | DOMAIN | 228 | 253 | 9 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 254 | 277 | 10 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| FT | DOMAIN | 278 | 285 | 11 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | TRANSMEM | 286 | 310 | 12 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| FT | DOMAIN | 311 | 400 | 13 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | DISULFID | 112 | 186 | 14 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| FT | BINDING | 297 | 297 | 15 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | LIPID | 323 | 323 | 16 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| FT | CARBOHYD | 5 | 5 | 17 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |
| FT | CARBOHYD | 196 | 196 | 18 (POTENTIAL). | EXTRACELLULAR (POTENTIAL). |
| SEQ | SEQUENCE | 400 AA; | 44946 MW; | 19 (POTENTIAL). | CYTOPLASMIC (POTENTIAL). |

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Query Match          12.9%; Score 252.5; DB 1; Length 400;
Best Local Similarity 26.8%; Pred. NO. 1.5e-10;
Matches    95; Conservative   48; Mismatches 147; Indels    65; Gaps    11;

OY      16 SPL---TAFELKLT-SLGEIIGSVVGNLLISILAVKDKTLNHPAPYFLIDCCSDILRSA 71
       ||| ||| : : : | : |||| : : | : | : | : | : | : | : | : | : |
DB      31 APLFEPFAVERIALLLGGALLGVGNNLLVLLIKPRLRPHLLFVLNLSIGDLVSL 90
OY      72 ICFPPVENVS-VKNGSTWTGYTLCKVIAPFLGVLSGFHTAFMFCISVTRYTAIAHHRPT 130
       ||| ||| : : : | : |||| : : | : | : | : | : | : | : | : | : |
DB      91 FGWETPFASCLRNQ--VWDMDAGCAMDEFGSGLSFGFSITTLTVLAVERIRIVHARV-- 146
OY      131 KRLFWTCGLATICMWTLTSVMAAFRPVLDVGYSITIREDOCTPHRSFRANDSIFML 190
DB     147 --INFSWAMRAITYIMLYSLMAGAPLLGMNRYIIDHGLCGTYDWRSKDADS--SFYL 203
OY      191 LALILATOLAYLKLIFFVHRRKKRPVOFAAAYSQNTFHGPCASGOAAANMLLAGFGRG 250
DB     204 LFGLGLVV-----PGILA-----HCYG----- 221
OY      251 PTPPLLGIROMANTTGRRRLVIDEFMEKRISMFIINTFLTLLMGPLYLVACWYWF 310
       ||| ||| : : : | : |||| : : | : | : | : | : | : | : | : | : |
DB     222 --HLIYSVRMLRCVEDLOTIOVIMLEHYEKRVAKMCMAFVELTCWMPIYTRBELVN 278
OY      311 ARGPVPGSGFLTAVMMSFQAQINPEFCISNRRLR-----CFSTLLYCRK 359
DB     279 GYGHLPVTFVSIVSYLFPAKSSVYNPVILYIPMNRRFRSLQLLCF--RLRRCOR 331

RESULT 15
ALAA_ORYLA
ID ALAA_ORYLA STANDARD; PROT; 470 AA.
AC Q91117;
DT 01-NOV-1997 (Rel. 35, Created)
DR 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha-1A adrenergic receptor (MAR1).
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphia; Altheriomorpha;
OC Belontiiformes; Adrianchichthyidae; Oryziinae; Oryzias.
NC NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184522; PubMed=8654394;
RA Yasuoka A., Abe K., Arai S., Emori Y.;
RT "Molecular cloning and functional expression of the
  alpha1A-adrenoceptor of Medaka fish, Oryzias latipes.";
  Eur. J. Biochem. 235:501-507(1996).
CC -!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CALCIN SECOND MESSENGER SYSTEM (BY SIMILARITY).
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CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D63859: BAA09921.1; -
DR GCRDB: GCR_1567; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 27
FT TRANSSEM 28 51
FT DOMAIN 52 64
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OM protein - protein search, using sw model

Run on: July 19, 2002, 14:39:19 ; Search time 28.54 seconds

(without alignments)
2242.751 Million cell updates/sec

Title: US-09-698-419-14
Perfect score: 1963
Sequence: 1 MANYSHADNITLONLSPLTA.....STLLXCRKRLPREPCVI 370

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-REMBL_19:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Length | DB | ID | Description |
|------------|-------|---------|--------|----|--------|---------------------|
| 1 | 250 | 12.7 | 471 | 11 | Q9QW77 | Q9QW77 cricetus |
| 2 | 247.5 | 12.6 | 396 | 4 | O92492 | O92492 homo sapien |
| 3 | 246.5 | 12.6 | 447 | 4 | O16144 | O16144 homo sapien |
| 4 | 243.5 | 12.4 | 378 | 4 | O96KH9 | O96KH9 homo sapien |
| 5 | 243.5 | 12.4 | 387 | 4 | O96K10 | O96K10 homo sapien |
| 6 | 240.5 | 12.3 | 396 | 4 | O75824 | O75824 homo sapien |
| 7 | 238.5 | 12.1 | 571 | 6 | O9TWM9 | O9TWM9 sus scrofa |
| 8 | 236.5 | 12.0 | 419 | 5 | O77254 | O77254 boophilus m |
| 9 | 236.5 | 12.0 | 436 | 11 | O9DBV6 | O9DBV6 mus musculu |
| 10 | 235.5 | 12.0 | 515 | 11 | O9DBL0 | O9DBL0 mus musculu |
| 11 | 234 | 11.9 | 405 | 11 | O9CNR2 | O9CNR2 mus musculu |
| 12 | 234 | 11.9 | 414 | 6 | O9GKAO | O9GKAO canis famill |
| 13 | 234 | 11.9 | 414 | 6 | O9GK99 | O9GK99 canis famill |
| 14 | 233.5 | 11.9 | 466 | 4 | O96RE8 | O96RE8 homo sapien |
| 15 | 233 | 11.9 | 422 | 6 | O9N297 | O9N297 gorilla gor |
| 16 | 233 | 11.9 | 422 | 6 | O9N296 | O9N296 pongo pygma |

| | | | | | | |
|----|-------|------|-----|----|--------|---------------------|
| 17 | 233 | 11.9 | 470 | 11 | P97842 | P97842 rattus norv |
| 18 | 231 | 11.8 | 440 | 5 | O9N324 | O9N324 ctenorhabi |
| 19 | 231 | 11.8 | 450 | 11 | P89005 | P89005 praeomys nat |
| 20 | 231 | 11.8 | 508 | 5 | O9VC23 | O9VC23 drosophila |
| 21 | 230.5 | 11.7 | 394 | 5 | O9NHE3 | O9NHE3 aplisys cal |
| 22 | 230 | 11.7 | 422 | 6 | O9N298 | O9N298 pan troglod |
| 23 | 230 | 11.7 | 462 | 4 | O9H849 | O9H849 homo sapien |
| 24 | 230 | 11.7 | 516 | 4 | O96LC6 | O96LC6 homo sapien |
| 25 | 229 | 11.7 | 355 | 13 | O9W615 | O9W615 latimeria c |
| 26 | 229 | 11.7 | 417 | 11 | O924H0 | O924H0 mus musculu |
| 27 | 228 | 11.6 | 394 | 4 | O9NJS6 | O9NJS6 aplisys kur |
| 28 | 227.5 | 11.6 | 402 | 13 | O9OX46 | O9OX46 brachydanio |
| 29 | 227.5 | 11.6 | 455 | 4 | O60451 | O60451 homo sapien |
| 30 | 226 | 11.5 | 516 | 4 | O9NKT7 | O9NKT7 homo sapien |
| 31 | 224.5 | 11.4 | 518 | 6 | O9NWT8 | O9NWT8 oryctolagus |
| 32 | 224 | 11.4 | 399 | 5 | O9NG02 | O9NG02 apis mellif |
| 33 | 223.5 | 11.4 | 355 | 13 | O9IA35 | O9IA35 poephila gu |
| 34 | 223 | 11.4 | 445 | 4 | O9NZR3 | O9NZR3 homo sapien |
| 35 | 222.5 | 11.3 | 405 | 11 | O924N0 | O924N0 mus musculu |
| 36 | 222.5 | 11.3 | 429 | 4 | O13729 | O13729 homo sapien |
| 37 | 222.5 | 11.3 | 464 | 13 | O9OWQ6 | O9OWQ6 oncorhynch |
| 38 | 222.5 | 11.3 | 499 | 4 | O13675 | O13675 homo sapien |
| 39 | 222 | 11.3 | 443 | 4 | O9UPA9 | O9UPA9 homo sapien |
| 40 | 222 | 11.3 | 461 | 13 | O9OWQ7 | O9OWQ7 oncorhynch |
| 41 | 221.5 | 11.3 | 466 | 4 | O9UP63 | O9UP63 homo sapien |
| 42 | 221 | 11.3 | 310 | 13 | O91973 | O91973 serinus can |
| 43 | 220.5 | 11.2 | 430 | 4 | O96RN3 | O96RN3 homo sapien |
| 44 | 220 | 11.2 | 559 | 11 | O9QW71 | O9QW71 rattus sp. |
| 45 | 219.5 | 11.2 | 464 | 5 | O9GQ54 | O9GQ54 aedes aegy |

ALIGNMENTS

RESULT 1
ID Q9QW77 PRELIMINARY; PRT; 471 AA.
AC Q9QW77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 5-HT2 RECEPTOR-SEROTONINERGIC RECEPTOR.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92049369; PubMed=1944295;
RA Van Obberghen-Schilling E., Voutet-Craviari V., Haslam R.J.,
Chambard J.C., Pouyssegur J.;
RT "Cloning, functional expression and role in cell growth regulation of
a hamster 5-HT2 receptor subtype";
RL Mol. Endocrinol. 5:881-889(1991).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1. 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1, 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_FL_2, 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 471 AA; 52856 MW; 2575357886944867 CRC64;

Query Match 12.7%; Score 250; DB 11; Length 471;
Best Local Similarity 23.8%; Pred. No. 6.7e-16;
Matches 84; Conservative 69; Mismatches 150; Indels 50; Gaps 13;

OY 30 IIVSVVGNLILSLVKDKTLRAPPYFLDLCCSILSAICFPVFNYSVKNGSTWY 89
DB 84 VILITAGNLTIVMAVSLERKIONATNYFILMSIAIDMLGLFVMPVSMILTYGWPPI 143

QY 90 GTLCKVIAFLVLSCTFTAFMLFCISTVRYLAIA----HHRFTKRLTFMTCLAVICMV 145
 DB 144 PSKCAWVIYLDVIFSTASIMILCALISDRYVALIONPIHHSFNSTKFLKIA-----V 199
 QY 146 WFLSVAMAF-PVLDVGYTSFTREDDQCTFQHRSPRANSLGFMILLAILATQCLVYK 204
 DB 200 WTISVGSMPPIPVFGLQDDSKVFKQSGCLL-----ADNN--FVLIGSVAFEPFITIMV 251
 QY 205 LIEFPHDRKKPKPVGFVAASQNTMTHFGGASGOAANMLAGRGRTPEPTLIGI----- 259
 DB 252 ITYEF-----TKSLQKEATLC-----VSDLSTRAKLAFSPF--LPQSSLSSEKLFQ 296
 QY 260 ----RONANTGRRRLVLVDEFKMEKRISRMFYIMTFLFLTMGPYLVACYWRFAR---- 312
 DB 297 RSIHPEPSYIGR---TMOSISNROACKVIGIVFELFVVMCPEFININAMVICKESC 353
 QY 313 GPVPGGFLTAAVWMSFAOAGINPVCIFSNRELRCSTLLIYC--RKSRLP 363
 DB 354 NEHVIGALLNFWGIVGLSSAVNPVLYTLFNKTYSAFS-RYIQCQYKENRFP 405
 RESULT 2
 ID 092492 PRELIMINARY: PRT: 396 AA.
 AC 092492:
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CHOLECYSTOKININ-B RECEPTOR/GASTRIN RECEPTOR (CCR-B GASTRIN RECEPTOR ISOFORM) (FRAGMENT).
 DE CCKBR OR CCK-B.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RC MEDLINE=93352657; PubMed=8349705;
 RA Ito M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima N., Nakata H., Chiba T., Chihara K.;
 RT "Functional characterization of a human brain cholecystokinin-B receptor. A trophic effect of cholecystokinin and gastrin.";
 RL J. Biol. Chem. 268:18300-18305(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RC MEDLINE=94038108; PubMed=8222757;
 RA Zimonjic D.B., Popescu N.C., Matsui T., Ito M., Chihara K.;
 RT "Localization of the human cholecystokinin-B/gastrin receptor gene (CCKBR) to chromosome 11p15.5--p15.4 by fluorescence in situ hybridization.";
 RL Cytogenet. Cell Genet. 65:184-185(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RC MEDLINE=95151633; PubMed=7848914;
 RA Ito M., Iwata N., Taniguchi T., Murayama T., Chihara K., Matsui T.;
 RT "Functional characterization of two cholecystokinin-B/gastrin receptor isoforms: a preferential splice donor site in the human receptor gene.";
 RL Cell Growth Differ. 5:1127-1135(1994).
 RN [4]
 RP SEQUENCE OF 16-26 FROM N.A.
 RX MEDLINE=95194412; PubMed=7887934;
 RA Miyake A.;
 RT "A truncated isoform of human CCK-B/gastrin receptor generated by alternative usage of a novel exon.";
 RL Biochem. Biophys. Res. Commun. 208:230-237(1995).
 DR EMBL: D21219; BAA04759.1;
 DR EMBL: S76072; AAB33740.1;
 DR HSSP: P02699; 1F88.

DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
 FT NON_TER 396 396
 SQ SEQUENCE 396 AA; 43252 MW; A25D5597CA903C0 CRC64;

Query Match 12.6%; Score 247.5; DB 4; Length 396;
 Best Local Similarity 24.7%; Pred No. 9.6e-16;
 Matches 101; Conservative 48; Mismatches 145; Indels 115; Gaps 16;

QY 22 LKTSGLFIIGSVVGNLLSILVYKDLHRAHYFLDLCCSDILRSALICEPEVNSV 81
 DB 5 IRTLVAVIFMISVGNMILITVVLGSLRRLFTVNAFLSLAVSDLLAVACHEFTLLPN 64
 QY 82 KNGSTWYTGTLCKVIAFLVLSCTFTAFMLFCISTVRYLAIAHHRFTKRLTFWT---- 137
 DB 65 LMG-TFIFGVICKAVSYLGVSVSTSLVAIALERSAICR---PLQARVWQTRSH 119
 QY 138 CLAVICMWTLVAMAF-PVLDVGYTSFTREDDQCTFQHRSPRANSLGFMILL 192
 DB 120 AARVIVATMLSLGLMVPYV-----YTVVQPVGPVYLQCVHKRPSARVQTSVLLLL 174
 QY 193 LIL-----LATOLYLLKLIIF-----FVHRRKKRPVQFV 221
 DB 175 LFTIPGVMAVAAGLSRELTLGRFDGSDSDSVNRNQGGLPAVHNGRCRPE--T 232
 QY 222 AAYSON-----WTFHGPAGSGAANMLAGFGGCPPTPTLLIGIRON 262
 DB 233 GAAGEDSDGCVYOLPPSRPALLETALTPAPGS-----GSRPTQAKLA--- 276
 QY 263 ANTTGRRRLVLVDEFKMEKRISRMFYIMTFLFLTMGPYLVACYWRFARGP-----VVP 318
 DB 277 -----KKVAVNMLVIVVFLFLCMLPYVSANTWRP-DGPGAHRLSG 318
 QY 319 GFLTAAVWMSFAOAGINPVCIFSNRELRC-STSTLLYCKRSRLPREP 366
 DB 319 APSIFHLISYASACVNPVLYCCFMHRRFRQACLETQARCC-----PRP 362
 RESULT 3
 ID 016144 PRELIMINARY: PRT: 447 AA.
 AC 016144:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CHOLECYSTOKININ B RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RC MEDLINE=94241526; PubMed=8185170;
 RA Herget T., Setälä T., Wu S.V., Walsh J.H., Rozengurt E.;
 RT "Cholecystokinin stimulates Ca2+ mobilization and clonal growth in small cell lung cancer through CCKA and CCKB/gastrin receptors.";
 RL Ann. N. Y. Acad. Sci. 713:283-297(1994).
 DR EMBL: S70057; AAB30766.2;
 DR HSSP: P02699; 1F88.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
 KW Receptor. 447 AA; 48418 MW; E3DAAE5EE10FB999 CRC64;
 SQ SEQUENCE

Query Match 12.6%; Score 246.5; DB 4; Length 447;
Best Local Similarity 24.7%; Pred. No. 1.4e-15;
Matches 101; Conservative 48; Mismatches 145; Indels 115; Gaps 16;

QY 22 LKLSIGFIIGSVGNLISILVADKTHRAPIYFLDLCCSDIRSAICPFVNSV 81
DB 56 IRTTAVAVELMSVGNMILVGLSRRLRTVNAFLSLAVSDLLAAVACMPFTLPN 115
QY 82 KNGSTWTCGLCKVAFGLVLSCTPHAFMLFCISVTRTALAHHRRTYRRLFWT 137
DB 116 LMG-FFIFETVICKAVSYLMGVSSTLSVAIALERYSALICR-PLQARWQRRSH 170
QY 138 CLAVICMWTLSSVAAFP-PVLDTGYSTFREED--OCTFHRSERANDSLGEMLLA 192
DB 171 AARVIAVATLLSGLLANVPV-----YTVQPVGPRLQGVHRRPSARVQTSVLLLL 225
QY 193 LIL-----LATOLVYLKIF-----FVHRRKKRPVOFV 221
DB 226 LEFIPGVNAVAVGLISRELTLGRFDGSDSDSQRVRNQGILPQAVHONGRCRPE-T 283
QY 222 AAVSON-----WTFHGPASGQAANWLAGFGGCPFPPELLGITRON 262
DB 284 GAVGKSDGCVYOLPSPRALLETALTAPGPGS-----GSRPTQAKLA---- 327
QY 263 AMTGRRLVLVDEFKMERISRMFIYIMFLFLMGPVLVACWRYFARGP---VYVG 318
DB 328 -----KRVVAMLLIVYVFLCMLPVSANTWRAP-DGPGAHALSG 369
QY 319 GFLTAVMWSFAQAGINPVCIPSPNRELRR-CFSTLLYCKRSRLPREP 366
DB 370 APTSFHLLSYASACVNPVLYCGMHRFRQACLETARCC-----PRPP 413

RESULT 4
ID 096KH9 PRELIMINARY; PRT; 378 AA.
AC 096KH9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 5-HYDROXYTRYPTAMINE4 RECEPTOR.
GN HTR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP TISSUE=BRNIN (HIPPOCAMPUS);
RC SEQUENCE FROM N.A.
RA Villaro M.T., Domenech T., Palacios J.M., Mengod G.;
RT "Cloning and characterization of multiple human 5-HT4 receptor
variants including a novel variant that lacks the alternatively
spliced C-terminal exon."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ278981; CAC22250.1;
KW Receptor.
SQ SEQUENCE 378 AA; 42745 MW; E45038EF832270D CRC64;

Query Match 12.4%; Score 243.5; DB 4; Length 378;
Best Local Similarity 22.7%; Pred. No. 2.2e-15;
Matches 88; Conservative 64; Mismatches 152; Indels 83; Gaps 13;

QY 9 DNILQNLSPPLAF-----LKLSIGFIIGSVGNLISILVADKTHRA-APYFLDL 61
DB 2 DKLDANVSEBEGFSGVERKVVLLFTSLVIMALGNLWVAVCMQRDLRIKTNIFYVS 61
QY 62 LCCSDILRSALICPF- VENSVKNGSTWYGTLLCKVIAFLVLSCTPHAFMLFCISVTRY 120
DB 62 LAFADLLVSVLMPGALIELVOD--IMWGEVCLVTRTSLDVLTLTASIFHLCCISIDRY 119
QY 121 LAI-AHHRFTYRRLTFWTCCLAVICMWTLSSVAAFPVL---DVGTSYSTRBEDCTQF 175

DB 120 YALCCOPLVYNNKMTPLRIALMLGCGWVTPFISFLPMOGNNIGIIDL-----E 171
QY 176 HRSEFRANDS-----LGMILLALLILALQVLYLKLIFVHDKRKKMP 217
DB 172 KRKFNONSNSTYCVFMWVKPYATCSVAFYIPFLIMVLAAYRIVTAKENAHQIOMQR 231
QY 218 VQFAAVASQNTFHPGASGQAANWLAGFGGCPFPPTLLGITRONANTGRRRLVLDEF 277
DB 232 A-----GASSESRL-----QSADQSHTRM----- 251
QY 278 KMERISRMFIYIMFLFLMGPVLVACWRYFARGPVGFLTAAMWSAQAGINPF 337
DB 252 RTEFKAKTLCTIIGCFCLCAAPFVTNIYDPEI-DYTVPGQVWTAFLMLGYINSGLNPF 310
QY 338 VCISNRELRCFSTLLYCKRSRLPR 364
DB 311 LYAFNLKSFRRAP-LIILCDDERYRR 336

RESULT 5
ID 096KIT0 PRELIMINARY; PRT; 387 AA.
AC 096KIT0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 5-HYDROXYTRYPTAMINE4 RECEPTOR.
GN HTR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP TISSUE=BRNIN (HIPPOCAMPUS);
RC SEQUENCE FROM N.A.
RA Villaro M.T., Domenech T., Palacios J.M., Mengod G.;
RT "Cloning and characterization of multiple human 5-HT4 receptor
variants including a novel variant that lacks the alternatively
spliced C-terminal exon."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ278979; CAC22248.1;
KW Receptor.
SQ SEQUENCE 387 AA; 44109 MW; 43019BED75AC9D0F CRC64;

Query Match 12.4%; Score 243.5; DB 4; Length 387;
Best Local Similarity 22.7%; Pred. No. 2.3e-15;
Matches 88; Conservative 64; Mismatches 152; Indels 83; Gaps 13;

QY 9 DNILQNLSPPLAF-----LKLSIGFIIGSVGNLISILVADKTHRA-APYFLDL 61
DB 2 DKLDANVSEBEGFSGVERKVVLLFTSLVIMALGNLWVAVCMQRDLRIKTNIFYVS 61
QY 62 LCCSDILRSALICPF- VENSVKNGSTWYGTLLCKVIAFLVLSCTPHAFMLFCISVTRY 120
DB 62 LAFADLLVSVLMPGALIELVOD--IMWGEVCLVTRTSLDVLTLTASIFHLCCISIDRY 119
QY 121 LAI-AHHRFTYRRLTFWTCCLAVICMWTLSSVAAFPVL---DVGTSYSTRBEDCTQF 175
DB 120 YALCCOPLVYNNKMTPLRIALMLGCGWVTPFISFLPMOGNNIGIIDL-----E 171
QY 176 HRSEFRANDS-----LGMILLALLILALQVLYLKLIFVHDKRKKMP 217
DB 172 KRKFNONSNSTYCVFMWVKPYATCSVAFYIPFLIMVLAAYRIVTAKENAHQIOMQR 231
QY 218 VQFAAVASQNTFHPGASGQAANWLAGFGGCPFPPTLLGITRONANTGRRRLVLDEF 277
DB 232 A-----GASSESRL-----QSADQSHTRM----- 251
QY 278 KMERISRMFIYIMFLFLMGPVLVACWRYFARGPVGFLTAAMWSAQAGINPF 337
DB 252 RTEFKAKTLCTIIGCFCLCAAPFVTNIYDPEI-DYTVPGQVWTAFLMLGYINSGLNPF 310

OY 338 VCIFSNRELRCFSTLLTYCRSLRP 364
DB 311 LYAFLNKSFERRAF-LIILCCDDERRR 336

RESULT 6

ID 075824 PRELIMINARY; PRT; 396 AA.

AC 075824;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE GASTRIN\CHOLECYSTOKININ BRAIN RECEPTOR (FRAGMENT).
GN CCKBR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99087707; PubMed-9872672;
RA O'Brian K.C., Ali S.Y., Meier H.U.G., Bepler G.;
RT "An 84-kilobase physical map and repeat polymorphisms of the
RT gastrin/cholecystokinin brain receptor region at the junction of
RT Chromosome segments 11p15.4 and 15.5";
RL EMBL; AF074029; AAC27510.1;
DR EMBL; AF074035; AAC27510.1; JOINED.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECP_FL2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 396 AA; 43286 MW; 54BB9A8D0257C4E5 CRC64;

Query Match 12.3%; Score 240.5; DB 4; Length 396;
Best Local Similarity 24.2%; Pred. No. 4.5e-15;
Matches 99; Conservative 49; Mismatches 146; Indels 115; Gaps 16;

OY 22 LKTLGFIQSVGNLLISILVKKDKTLHRAPIYFLDLCCSDILRSALCPPEVFNVS 81
DB 5 IRTLYAVFELMSVGNMIIIVLGLSRRLRTVNAFLSMASDILLAVACMPFTLLPN 64
OY 82 KNGSWTGTGLCKYIAFLGVLSCEFTAFMLPCISTRYLIAIHHRFYTKRLTFWT 137
DB 65 IMG-FFIGETVICKAVSYLMGVSYSVSLVALALERSAICR---PLQARVQOTRSH 119
OY 138 CLAVICMWTLSVMAAF-PVLDDVGTYSFIREED---OCTFOHRSFRANDSLGEMLLA 192
DB 120 AARVAVATMLSLGLMVPFV-----YTVQPRPVRLDQVHWPBARVQOTSVLLIL 174
OY 193 LIL-----LATQVLYKLIF-----FVHDKRMKPVQV 221
DB 175 LFFIGVMAVAVYGLISRELTYGLRPDGDSDSDQSRVRNOGLPQAVHONGCRPE--T 232
OY 222 AAVSON-----WTFHGPAGSGOAAANMLAGFGRGPPPTLLGIRON 262
DB 233 GAVGSDGDCYVOLPRSPALLETALTALAPGGS-----GSRPQAKILA--- 276
OY 263 AATTGRRRLVLDEFMERISRMFYIMTFLFTLMGPYLAVACYWVFARGP---VVP 318
DB 277 -----KRRVARMILVIVLFLCMLPYASANTWAF--DGPANHRLSG 318
OY 319 GFLTAVMWSFAQAGINPVCIFSNELRR-CESTLLTYCRSLRP 366
DB 319 APLSTHLLSYASACVNPVLYGCMHRRROACLETCAKCC---PRP 362

RESULT 7
OY 97TW9

ID 097TW9 PRELIMINARY; PRT; 571 AA.
AC 097TW9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ALPHA-1D ADRENERGIC RECEPTOR.
GN ALPHA-1D.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]
RP SEQUENCE FROM N.A.
RA Uhlen S., Wraath A.;
RT "Characterization of the pig alpha-1D adrenergic receptor";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBD databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ250492; CAB59347.1; JOINED.
DR EMBL; AJ250493; CAB59347.1; JOINED.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 571 AA; 60698 MW; BACFFB5C903972B1 CRC64;

Query Match 12.1%; Score 238.5; DB 6; Length 571;
Best Local Similarity 24.3%; Pred. No. 1.1e-14;
Matches 89; Conservative 61; Mismatches 161; Indels 47; Gaps 12;

OY 27 LGEFIQSVGNLLISILVKKDKTLHRAPIYFLDLCCSDILRSALCPPEVFNVS 86
DB 102 LAEFLTAAGNLLVITSVACNRRLQVTNFTYNAVADLLSATVLPFATHEVLG-F 160
OY 87 WYGTTLCKVIAFLGVLSCEFTAFMLPCISTRYLIAIHHRFYTKRLTFWTCLAVICMW 146
DB 161 WARGRACDVAWADVCTASILCTISDVYGVHSHKYPISMTERRAAAILALWM 220
OY 147 TLSVMAFPVYL-----DVGTYSFIREDOCTPOHRSFRANDSLGEMLLAILLAT 198
DB 221 AVAIVSVGGLLKEKPEPPDERECGITEAGYAVF-----SLCSFYLPMAVIV--- 270
OY 199 QLVLYKLIFVHDKRMKPVQVFAVSONMTFHGPAGSGOAAANMLAGFGRGPPPTLLG 258
DB 271 -VMICRV--IVVASTTRSLR--AGVARE-----RGKASEVYLRIHCGSSGTIDRG 317
OY 259 ---IRONANTTGRRL-LVDEFMERISRMFYIMTFLFTLMGPYLAVACYWVFARGP 314
DB 318 HGAMRSTKGTFRSSLSRLRKFRKKAKTLAIVGVFLCWFPPFF-----VPLG 372
OY 315 VVP-----GGFLTAVMWSFAQAGINPVCIFSNELRCFSTLL-LYCRSLRP 366
DB 373 LFPOLKPEGVFKVIFWLGYSNCVNPDIYCSSREFKRAFLRLRCOCHHSRRRRRP 430

RESULT 8
ID 077254 PRELIMINARY; PRT; 419 AA.
AC 077254;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N-STRAIN; TISSUE=LARVA;

RA Baxter G.D., Barker S.C.;
RT "Isolation of an octopamine-like, G-protein coupled receptor cDNA from
the cattle tick, Boophilus microplus";
RL Insect Biochem Mol Biol. 29:461-467(2000).
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: A010743; CA09335.1; -
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPEP_FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 419 AA; 47090 MW; 8DEDCAE2E50F3FA5 CRC64;

Query Match 12.0%; Score 236.5; DB 5; Length 419;
Best Local Similarity 23.5%; Pred. No. 1.2e-14;
Matches 89; Conservative 60; Mismatches 162; Indels 67; Gaps 13;

QY 26 SLGFIIGSVAGNLLISILVKKOTLRADYFLLDCCSDILRSACFPF-VENSVMKNG 84
DB 63 SLSTFIVFVGVNVLVCSVFENHRPLRTVQNVFLSLADIAVALLVMPENVAYSIW- 120
QY 85 STWTYGLTCKVIAFLGVLSCFHTAFMLFCISTRYLAIAHHRFYTKRLTWTCLAVICM 144
DB 121 GRNVFELHCELMVCDVLCCTASTILMLCAIDRYAHHDPYVAKRLRLVLLSTFL 180
QY 145 VVTLVSAAAFPPVLDVGYTSFIREDOCTFOHRSFRANDSLGFMLLA-----LILLATQ 199
DB 181 VVWISALISVPL-IGMNMWPEQFDETT-----PCRLTQEGYVLYSAGSFFIPLIMS 234
QY 200 LVYTLKLFVHDKRK------PVQVFAVVSQNTFHGPGAS----- 236
DB 235 IYVLT-FLATRRRLERANAATAKVPSSATRCATVEHSVALDQ--RPPSSSEPP 289
QY 237 ----GGAAMWLAGFGGFPPLLLGRQANNTG-----RRLLVLDKRMKRI 283
DB 290 PQRGGOTTE-----RPSIADTSVYLEONGRPSPVKTFCWEORORI-----SLSRERRA 339
QY 284 SRMFYIMTFELTLMGPRYLACVYRWVAFRGVPGFLTAVMWSPFQAGINPFVCFISN 343
DB 340 ARLGLVAGVFCVLCMPFLIMYTAFAFCDCVSDRLVNFITWLGIVNSALNPIYVEN 399
QY 344 RELRCFSTLLYCKRSR 361
DB 400 TDFRAFRS--LLCSGNR 415

RESULT 9
Q9DBV6 PRELIMINARY; PRT; 436 AA.
AC Q9DBV6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ADULT MALE LUNG CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:1200012013, FULL INSERT SEQUENCE.
GN CCKAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aizawa K., Izawa K., Nishii K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., Ring B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsunki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
DR EMBL: AK004730; BAB3512.1; -
DR HSSP: P02699; 1F88.
DR MGD: MGI:99478; Cckar.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECPEP_FL2; 1.
SQ SEQUENCE 436 AA; 48446 MW; 49B4AD57E080708A CRC64;

Query Match 12.0%; Score 236.5; DB 11; Length 436;
Best Local Similarity 23.3%; Pred. No. 1.2e-14;
Matches 95; Conservative 67; Mismatches 171; Indels 75; Gaps 13;

QY 9 DNILQNSPL------AFKLTSLGFIIGSVAGNLLIS 43
DB 5 DSLNNGSNITPPCELGENETLFCIDOPHPKESQMSAVQIILSYIFSLVIGDLYVT 64
QY 44 LVVCKTTHRAPYVLLDCCSDILRSACFPF-VENSVMKNGSTWTGTLCKVIAFLG 101
DB 65 VLIRKRRRTYNTIFLLSLAVSDMLCLPCMPFNILPILNKO--FIRSAVCKTTTYPM 121
QY 102 VLSCFHTAFMLFCISTRYLAIAHHRFYTKRLTFT-----CLAVICMWTLSVAAFPV 157
DB 122 GTSVSVSTFNLVALISLEHYGAIC--RPLQSRV--WQTSKALKVIAATMCLSTFTIMTP 177
QY 158 LDVGTSFIREDO-----CTFOHRSFRANDSLGFMLLALL-----ANQVYTLKI 206
DB 178 IYSLVLPPTKNNQNTANNCREFLPDAMQSQTFLLILFLIPGVVYVAYGLISLEL- 236
QY 207 FFVHDKRMKPVQVFAVVSQNTFHGPGASGGAANMLAGFG--RGTPPPLLLGRONA 263
DB 237 ---YQIKFPDASOKSAKREKRLSSGGGGSSSSRYEDSDCYQKSRPKRLLEQQLS 293
QY 264 NTGRRRL-----LVLDKRMKRLSRMFYIMTFELTLMGPRYLACVYRWV-- 310
DB 294 TSSSGRINRIRSSGSANLI-----AKRYIRMLIYIVLFFLCMPPIFSANARAYDT 348
QY 311 -ARGPVVPGFLTAVMWSPFQAGINPFVCFISNRELRCFSTLLYC 357
DB 349 VSAEKHLSTGPISTILLISTYSSCVNPIYCFMNRFRGLGFATPCC 396

RESULT 10
Q9DBLO PRELIMINARY; PRT; 515 AA.
AC Q9DBLO;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ADRENERGIC RECEPTOR, ALPHA 1B.
GN ADRA1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN NCB1
RP [1]

RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=LIVER;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momhaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL, AK004891; BAB3647.1;
DR HSSP; P29274; 1MMH.
DR MGI; MGI:104774; Adrb1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
KW SEQUENCE 515 AA; 56497 MW; 69D24E9978F81C1 CRC64;
SQ

Query Match 12.0%; Score 235.5; DB 11; Length 515;
Best Local Similarity 21.7%; Pred. No. 1.9e-14;
Matches 85; Conservative 65; Mismatches 173; Indels 69; Gaps 11;

QY 2 ANYSHADNLTQNLSPITAFATKTSAGFTIGV-----SVGNLISILVYDKTLHRAPIY 57
DB 23 ANFTGNQTSNSTLPQDVTTRAISVGLVGAFTLFAIVNITVLSVACRHLRTPTNY 82
QY 58 FLIDLCSDILRSACEPEFVNSKNGSTWYTGTLNCKVIAFLVGLSCFHAFMLFCISV 117
DB 83 FIVNLAIADLLSFTVLPVSATLEVIG-YVVLGRIFCDIMAAVDVLCCTISLCAISI 141
QY 118 TRYLAHHRFYTKRLFTWCLAVICWWTLSVMAFPVLDVGYTSFIRED-OCTFOH 176
DB 142 DRIQVRSYQVPTLVTRRAIILALSVWLSTYISIGPLL-GMKRPAPNDDECGVTE 199
QY 177 RSTR-NDSCIG-FMLLAILLANTQVYL-----KLIFVHDR 213
DB 200 EPPYALFSSSYEIPPLAVLWVCRYIAKRTTKMLGAVKEMSKNELLRISK- 258
QY 214 KMPVQFVAVSONMTHFGGASGQAANMLAGRGPTPTLLIGIONNTTGRRLV 273
DB 259 -----NHEDTLSTKA-----KGNPSSIAVR----- 282
QY 274 LDEFKMEKRISRMFYITFTFLMGVYLVACYWRVARGVVGGLTAAVMSFAOAG 333
DB 283 LEFSREKRAKAKTLGIVGFIICMLPFTALPLGSLFSTLKPRDPAVKVYVWLGYNESC 342
QY 334 INPVCIFSNRELRCFSTTL-LYCRKSLPR 364
DB 343 LNPILYPCSSKEKRAFMRIIGCCGCGRRRR 374

RESULT 11
Q9CRR2 PRELIMINARY; PRT; 405 AA.

AC Q9CRR2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
GN ADRENERGIC RECEPTOR, BETA 1 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=EMBRYONIC LUNG;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momhaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL, AK018378; BAB31185.1;
DR MGI; MGI:87937; Adrb1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
KW NON_TER 1
FT SEQUENCE 405 AA; 44741 MW; 4F0F3FB956BE2F4 CRC64;
SQ

Query Match 11.9%; Score 234; DB 11; Length 405;
Best Local Similarity 24.6%; Pred. No. 2e-14;
Matches 89; Conservative 63; Mismatches 150; Indels 60; Gaps 16;

QY 27 LGFTIGSVGNLISILVYDKTLHRAPIYFLDLCSDILRSACEPEFVNSKNGST 86
DB 4 LALIVLLVGNVAVIAIAATPRLQTLNLFINSASADLVGLVVPFGATVWVG-R 62
QY 87 WTYGTLCKVIAFLVGLSCFTAFELFC-ISTRYLAIAHHRFYTKRLFTWCLAVICV 145
DB 63 WEYSFCELTWTSVDL-CVTAASITELCVIALDRILATSPFRYSLLTRARARLVCTV 121
QY 146 WTLNVMAFPVLDVGYTSFIREDQ-----CTF-CHRSFR-ANDSIGMILLAL 193
DB 122 WAISALVSEFLPL---MHMRAESDEARCYNDPCDFVNRFAVAIASSVSVFVPLCI 178
QY 194 ILATQVLYLKLIFVHDRRKRPVQFVAVSONMTHFGGASGQAANMLAGRGPT- 252
DB 179 M-----AFYLVF-----REAKOVKTKDSCER-----RFLGGPAPRSP 214
QY 253 -----PPTLLGIRONANTGRR--RLTVDEFKMEKRISRMFYITFTFLMGVYLV 303
DB 215 EPSFSGPFRPADSIANCRSSKRPRSRVALREKALATLG-----INGVFLICMLPPL 270
QY 304 ACYWRVARGVVGGLTAAVWMSFAOAGINPV-CIFSRELRCFSTLLYCRKSL 362

Db 271 ANVKAHFR-DLVPRDLFEVFNMLGVANSAPNPIYC--RSPDRKAFQRLCCARRAC 327
 QY 363 PR 364
 Db 328 RR 329

RESULT 12

Q9GKA0 PRELIMINARY; PRT; 414 AA.
 ID Q9GKA0;
 AC Q9GKA0;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE DOPAMINE D2 RECEPTOR SHORT ISOFORM.
 GN DRD2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20510028; PubMed-11054572;
 RA Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
 RA Kaang B.;
 RT "Genomic analysis and functional expression of canine dopamine D2
 RT receptor."
 RL Gene 257:99-107(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF293962; AAC34495.1;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN RECP.F1.1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP.F1.2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 414 AA; 47289 MW; 7DAD2AD48621C074 CRC64;

Query Match 11.9%; Score 234; DB 6; Length 414;
 Best Local Similarity 21.2%; Pred. No. 2e-14;

Matches 83; Conservative 70; Mismatches 163; Indels 76; Gaps 12;

QY 24 LPSLGIIGSVVGNLLISILVKKTLHRAPIYFLDLCCSILRSALICFPFVNSVKN 83
 Db 41 LTLILFII---VGNVLVCAVSRKALQTTNTVLIYSLAVADLVATLVMPWVYLEV 97
 QY 84 GSTWYTGILTKVIAFLGVLSCHFTAFMLFCISVTRYLAIAHHRFYTKRLTFWTLAV-I 142
 Db 98 GE-WKFSRIHCDIFVTLDMVMTASILNLCASIDRYTAVAMPMLYNTRYSSKRRVTMI 156
 QY 143 CMWVTLVAMAFPPVLDVGTYSFIREDOCTFOHRSFRANDSLGFMILLALILATOLVY 202
 Db 157 AIVWVLSFTISCPILFGLNN---TDONECIIANPAFVYSSI---VSFYVPIVTLVLY 209
 QY 203 LKLIFFVHDRK-----MKPVQFAVAVSQNW----- 228
 Db 210 IKIYIVLRRRKRKRVNTERSSRAFRANLKAFLKEAARAQELMEMLSTSPERTRYSPI 269
 QY 229 -----TFHGPASGOAANWLAGFGGPTPTLLGI-----RONANT 265
 Db 270 PPSHQTLPLDPSSHGHSTADSPAKPEKN-GHAKDHPKIAKIFEQSMNGKRTSLKT 328
 QY 266 TGRRLVLVDEFKMEKRISRMFYIMTFLEFLTMGPYLVACYWRVAPVPGGFLTAAY 325
 Db 329 MSRRKL-----SQEKKATOMALIVGVFIICWLPFFTHILNHCECN-IPVLYSAFT 383
 QY 326 WMSFAQAGINPFCIFSNRELRCFSTLLYC 357
 Db 384 WLGVYNSAVNPILITYTFNIEFRKAF-LKILHC 414

RESULT 13

Q9GK99 PRELIMINARY; PRT; 414 AA.
 ID Q9GK99;
 AC Q9GK99;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE DOPAMINE D2 RECEPTOR SHORT ISOFORM.
 GN DRD2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20510028; PubMed-11054572;
 RA Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
 RA Kaang B.;
 RT "Genomic analysis and functional expression of canine dopamine D2
 RT receptor."
 RL Gene 257:99-107(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF293964; AAC34497.1;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN RECP.F1.1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP.F1.2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 414 AA; 47288 MW; 4E330ADC400FCB5C CRC64;

Query Match 11.9%; Score 234; DB 6; Length 414;
 Best Local Similarity 21.2%; Pred. No. 2e-14;

Matches 83; Conservative 70; Mismatches 163; Indels 76; Gaps 12;

QY 24 LPSLGIIGSVVGNLLISILVKKTLHRAPIYFLDLCCSILRSALICFPFVNSVKN 83
 Db 41 LTLILFII---VGNVLVCAVSRKALQTTNTVLIYSLAVADLVATLVMPWVYLEV 97
 QY 84 GSTWYTGILTKVIAFLGVLSCHFTAFMLFCISVTRYLAIAHHRFYTKRLTFWTLAV-I 142
 Db 98 GE-WKFSRIHCDIFVTLDMVMTASILNLCASIDRYTAVAMPMLYNTRYSSKRRVTMI 156
 QY 143 CMWVTLVAMAFPPVLDVGTYSFIREDOCTFOHRSFRANDSLGFMILLALILATOLVY 202
 Db 157 AIVWVLSFTISCPILFGLNN---TDONECIIANPAFVYSSI---VSFYVPIVTLVLY 209
 QY 203 LKLIFFVHDRK-----MKPVQFAVAVSQNW----- 228
 Db 210 IKIYIVLRRRKRKRVNTERSSRAFRANLKAFLKEAARAQELMEMLSTSPERTRYSPI 269
 QY 229 -----TFHGPASGOAANWLAGFGGPTPTLLGI-----RONANT 265
 Db 270 PPSHQTLPLDPSSHGHSTADSPAKPEKN-GHAKDHPKIAKIFEQSMNGKRTSLKT 328
 QY 266 TGRRLVLVDEFKMEKRISRMFYIMTFLEFLTMGPYLVACYWRVAPVPGGFLTAAY 325
 Db 329 MSRRKL-----SQEKKATOMALIVGVFIICWLPFFTHILNHCECN-IPVLYSAFT 383
 QY 326 WMSFAQAGINPFCIFSNRELRCFSTLLYC 357
 Db 384 WLGVYNSAVNPILITYTFNIEFRKAF-LKILHC 414

RESULT 14

Q9GRE8 PRELIMINARY; PRT; 466 AA.
 ID Q9GRE8;
 AC Q9GRE8;
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE ADENERGIC RECEPTOR ALPHA-1A.
 GN ADRA1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Banerjee A.G.N., Artl A.;
 RT "Rt-PCR cloning and sequence analysis of adrenergic receptor subtype-
 alpha-1a cDNA from human prostatic cell-line DU-145."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF395806; AAK77197.1;
 KW Receptor.
 SQ SEQUENCE 466 AA; 51431 MW; 876CBFB3E323B7A1 CRC64;

Query Match 11.9%; Score 233.5; DB 4; Length 466;
 Best Local Similarity 23.3%; Pred. No. 2,6e-14;
 Matches 90; Conservative 65; Mismatches 149; Indels 83; Gaps 15;

QY 8 ADNLQNTSPLE---AFKLTLGLFIVGVGNLLISILVYKDTLHRAPIYFLDCC 64
 DB 11 SSNCQPPAPVVISKAILLGLVGLLGLFVGNLIVLSVACHRLHSVTHRYIVNLAV 70
 QY 65 SDILSAICFPF--VENSVKNGSTWYGTLLCKVIAFLVLCGCFHAFMLFCISVTRYIA 122
 DB 71 ADLLTSLVLPESAIFEVY---GVNAFGHVFENIMAVAVDLCTASIMGLCISIDRYIG 127
 QY 123 IAHNFYTKRLTFWTCGLAVICMWTLSVMAFPVLDVGTYSFIREDOCTOHRSPRAN 182
 DB 128 VSHPLRYPTIVQIRGLNALLCVMAISLVSIGPLFG---WRQPAEDDTICO---IN 179
 QY 183 DSLGFMLLAL---ILLATOLVYLKLFVHDDR-----KMPVQFAVAVSON 227
 DB 180 EEPGVLVSALGSFYLPALIIIVMCRVYVAKRESRGKSGIKTKSSEQVTLAIHKR 239
 QY 228 WTEHGP-GASGOAANWLAGFGRGPTPLLLGIROMANTTGRRLLVLEDFKMKRISRM 286
 DB 240 ---NAPAGSGGMAKAKTTHFS-----VRLD---KFSEKKAAT 273
 QY 287 FYIMFLLTLTGPIVLVACYWRFVARGPVVPGGF-----LTAVMSFAQAGIN 335
 DB 274 LGIVGCEVLCWLPFLL-----VMPISGFEPPDERKSETVYKIVFWGLYMSGIN 322
 QY 336 PFVCFISNRELRCFSTTL--LYCRK 359
 DB 323 PIIFCSSQERKAFQNVLRIOCLCRK 349

RESULT 15
 Q9N297 PRELIMINARY; PRT; 422 AA.
 AC Q9N297;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SEROTONIN RECEPTOR 1A.
 GN HTR1A.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
 NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=GORILLA-01;
 RA Kitano T., Kobayakawa H., Saitou N.;
 RT "Silver Project."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL; AB041405; BAA94490.1;

DR HSSP; P29274; 1MH.
 DR InterPro; IPR000276; GPCR_Rhoopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 422 AA; 46154 MW; 012335E0403F1B90 CRC64;

Query Match 11.9%; Score 233; DB 6; Length 422;
 Best Local Similarity 20.9%; Pred. No. 2,6e-14;
 Matches 86; Conservative 72; Mismatches 170; Indels 84; Gaps 15;

QY 15 LSEPLT-AFLKTLN---LGFIVGVGNLLISILVYKDTLHRAPIYFLDCCSILIRSA 71
 DB 28 ISDVTSYGVITSLILGTLIFCAVGLACVYAAIALLERSLQNVANYVIGSLAVYDLNWSV 87
 QY 72 ICEPF-----VENSVKNGSTWYGTLLCKVIAFLVLCGCFHAFMLFCISVTRYIAAH 126
 DB 88 LVLPMAALYQVILNK-----WTIGQVYCDLFIALDVLCCTSSILHLCAIALDRYMAITDP 141
 QY 127 RFYTKRLTFWTCGLAVICMWTLSVMAFPVLDVGTYSFIREDOCTF-OHRSPRANDSL 185
 DB 142 IDYVKNRTPRAAALISITWLGFLISIPMLGKRPEDSDPDACISKHGTTITSTF 201
 QY 186 G-FMLLALILLATOLVYLKLFVHDDRKKKPVQFAVAVSONWTFHGP-----GASG 237
 DB 202 GARYIPLLLMLVLYGRIFRAAPRI--RKYVKVEKTEGADTRHGASAPQPKSVNGESG 259
 QY 238 QAANWLAGF-----GAGTPP-- 253
 DB 260 ---SRNRLGVESKAGALCANGAVROGDGALEVEVHARVNGSKHLPLPSEAGPTPCA 317
 QY 254 PTLGIROMANTTGRRLLVLEDFKMKRISRMFYIMFLLTLTGPIVLVACYWRFVARG 313
 DB 318 PASFERKNERNAKAKKMLAREKTYKTLG---LIMGFILLCWLPFVYALVLPCE 373
 QY 314 ---PVVPGGFLTAAVWMSFAQAGINPFVCFISNRELRCFSTTL--LYCRK 359
 DB 374 SCHMPTLLGAIIN---WLGYSNLSLNVIVAYFNKDKQNAFKLIKCKFCQ 422

Search completed: July 19, 2002, 14:43:05
 Job time: 226 sec

PS Example 1; Page 53-54; 72pp; Japanese.

XX The present sequence represents a G protein-coupled receptor protein,
CC designated SREB2. The protein is expressed in the central nervous
CC system. The SREB2 products are used for the diagnosis and treatment
CC of diseases of the central nervous system, including inflammatory
CC disorders of immunological origin.

XX Sequence 370 AA:

Query Match 100.0%; Score 1963; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e-208;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNLTQNLSPITAFILKLTSLGFIIGSVVGNLISILLVYKDTLHRAPIYFLL 60
DB 1 manyshadnltqnlspitafilkltslgfiigsvvgnllsillvkdktlhrapyfll 60
QY 61 DLCCSDILRSALCFPPFVNSVKNSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB dlccsdilrsalcfpfvnsvknstwygtlckviaflgvlscfhtafmlfcisvtry 120
QY 121 LAIAHHRFYTKRLTFWTCLAVICWMTLSVMAFPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 laiahhrfytkrltfwtclavicmwltsvmafppvldvgtysfiredoctfohrsfr 180
QY 181 ANDSLGFMILLALITATOLVYLKLIFFVHDKRKKMPVOFVAVSONMTFHPGASGOAA 240
DB 181 andslgfmillalitatolvylkliffvhdrrkmpvofvaavsonmtfhpgasgaa 240
QY 241 ANWLAGEGRGPTPTLLGIRONANTGRRRLVLDDEFKMERISRMFYIMTFLFLTMGP 300
DB 241 anwlaggrgptptllgironantgrrrlvlddefkmerisrmfyimtflfltlwgp 300
QY 301 YLVACYWVRVARGPVVPGGFLTAAMVMSFAOAGINPVCIFSRLRRCFSTLLCYCRKS 360
DB 301 ylvacywvrvargpvpggfltaamvmsfaaginpvcifsnrlrrcfstllcyckrs 360
QY 361 RLPREPYCVI 370
DB 361 rlprepycvi 370

RESULT 2

AAV30537
ID AAV30537 standard; Protein: 370 AA.

XX AAV30537;

DT 15-NOV-1999 (first entry)

DE A G protein-coupled receptor protein designated SREB2.

KW G protein-coupled receptor protein; SREB2; central nervous system;
KW inflammatory disorder; immunological.

XX Rattus sp.

XX MO9946378-A1.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-JP01191.

XX 12-MAR-1998; 98JP-0060245.

XX 03-FEB-1999; 99JP-0026774.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Matsunoto M, Sugimoto T, Takasaki J, Satto T, Kamohara M;
XX WPI; 1999-551407/46;

DR N-PSDB: AA210577.

XX G protein-coupled receptor proteins expressed in the central nervous
PT system and genes encoding them

XX Example 4; Page 66-67; 72pp; Japanese.

PS The present sequence represents a G protein-coupled receptor protein,
CC designated SREB2. The protein is expressed in the central nervous
CC system. The SREB2 products are used for the diagnosis and treatment
CC of diseases of the central nervous system, including inflammatory
CC disorders of immunological origin.

XX Sequence 370 AA:

Query Match 100.0%; Score 1963; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e-208;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNLTQNLSPITAFILKLTSLGFIIGSVVGNLISILLVYKDTLHRAPIYFLL 60
DB 1 manyshadnltqnlspitafilkltslgfiigsvvgnllsillvkdktlhrapyfll 60
QY 61 DLCCSDILRSALCFPPFVNSVKNSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB dlccsdilrsalcfpfvnsvknstwygtlckviaflgvlscfhtafmlfcisvtry 120
QY 121 LAIAHHRFYTKRLTFWTCLAVICWMTLSVMAFPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 laiahhrfytkrltfwtclavicmwltsvmafppvldvgtysfiredoctfohrsfr 180
QY 181 ANDSLGFMILLALITATOLVYLKLIFFVHDKRKKMPVOFVAVSONMTFHPGASGOAA 240
DB 181 andslgfmillalitatolvylkliffvhdrrkmpvofvaavsonmtfhpgasgaa 240
QY 241 ANWLAGEGRGPTPTLLGIRONANTGRRRLVLDDEFKMERISRMFYIMTFLFLTMGP 300
DB 241 anwlaggrgptptllgironantgrrrlvlddefkmerisrmfyimtflfltlwgp 300
QY 301 YLVACYWVRVARGPVVPGGFLTAAMVMSFAOAGINPVCIFSRLRRCFSTLLCYCRKS 360
DB 301 ylvacywvrvargpvpggfltaamvmsfaaginpvcifsnrlrrcfstllcyckrs 360
QY 361 RLPREPYCVI 370
DB 361 rlprepycvi 370

RESULT 3

AAV71303
ID AAV71303 standard; Protein: 370 AA.

XX AAV71303;

DT 02-NOV-2000 (first entry)

DE Human orphan G protein-coupled receptor hCHN3.

KW Human; orphan G protein-coupled receptor; GPCR; hCHN3; drug screening;
KW transmembrane receptor; expressed sequence tag; EST; signal cascade.

XX Homo sapiens.

XX WO200031258-A2.

XX 02-JUN-2000.

XX 13-OCT-1999; 99WO-US23687.

XX 20-NOV-1998; 98US-0109213.

XX 16-FEB-1999; 99US-0120416.
XX 26-FEB-1999; 99US-0121852.

PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-01223949.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0136567.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 29-JUN-1999; 99US-0141448.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156634.
PR 29-SEP-1999; 99US-0156653.
PR 01-OCT-1999; 99US-0157280.
PR 01-OCT-1999; 99US-0157281.
PR 01-OCT-1999; 99US-0157282.
PR 01-OCT-1999; 99US-0157293.
PR 01-OCT-1999; 99US-0157294.
PR 12-OCT-1999; 99US-0416760.
PR 12-OCT-1999; 99US-0417044.
PA (AREN-) ARENA PHARM INC.
XX Chen R, Dang HT, Liaw CW, Lin I;
XX WPI: 2000-400068/34.
DR N-PSDB; AAD01130.
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs
PT for use in the identification of G protein-coupled receptor agonists -
XX Claim 50; Page 74-75; 102pp; English.
XX The present amino acid sequence is the hCHN3, an endogenous human
XX orphan G protein-coupled receptor (GPCR), expressed in the foetal brain,
XX putamen and occipital cortex. The hCHN3 cDNA was identified using EST
XX (expressed sequence tag) 36581 as a probe.
CC The orphan GPCR of the invention, like all GPCRs has seven transmembrane
CC alpha helices with an extracellular N-terminus and an intracellular
CC C-terminus. However, no endogenous ligands has yet been identified for
CC the proteins of the invention. The orphan GPCRs may be used in the
CC identification of their endogenous ligands, and to screen potential GPCR
CC agonists and antagonists for use as pharmaceutical agents. The proteins
CC may also be used in the study of GPCR-mediated signalling cascades, and
CC to elucidate their precise role in normal and diseased human conditions.
CC Nucleic acid encoding human orphan GPCRs may be used for tissue
CC localisation expression analysis to provide information about their
CC function in healthy and pathological states.
XX
XX
SQ Sequence 370 AA;
Query Match 100.0%; Score 1963; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e-208;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MANYSHADNIIQNTSPYLAFLKLSLGIIGSVVGNLLISILYKDKTLHRAPIYFL 60
Db 1 manyshadniiqntspylafklslgllgsvvgnllisilylvkdktlhnapyfl 60
OY 61 DLCSDDILRSALCFPFVSVKNGSTWYGTITCKVIAFLGVLSCHPTAFMLCISVTRY 120
Db 61 dlcsddilrsalcfpfvsvkngstwygtitckviaflgvlschptafmlcisltry 120
OY 121 LAIAHRRYTKLTFWTCLAVICMWTLISVMAAPVLDVGYSFTRREDQCTFQHRSR 180
Db 121 laiahrrytklftwtclavicmwtlisvmaapvldvgysftrredqctfqrstr 180
OY 181 ANDSLGFMLLALLIATOLVYLLEFVHDBRKKKPVQFVAASQNMWTFHGSGASGOAA 240
Db 181 andslgfmllalliatalolvyllefvhdbrrkkpvaqfvaasqnmwtfhgsgasgaa 240
OY 241 ANWLAGFGRGPTPYLIGIRONANTYGRRLVLVDEFKMEKRISRPFYIMTFELTLWGP 300

Db 241 anwlagfgrgptpylligirnantygrrrllvldfkmekrisrmfymtfltlwgp 300
OY 301 YLVACYRWFAFGPVVGGFTAAVWMSFAOAGINPFCISNRELRCFSFTLLYCKRS 360
Db 301 ylvacyrwfavgpvvpggftaavwmsfaaglnpfcisnrelrcfstlllyckrs 360
OY 361 RLPREPYCVI 370
Db 361 rlprepycvi 370
RESULT 4
AAB02837
ID AAB02837 standard; Protein: 370 AA.
XX
AC AAB02837;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human: G protein coupled receptor hCHN3 protein SEQ ID NO:28.
XX
KW Human: G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.
XX Homo sapiens.
OS
XX
PN W0200022131-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99MO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121652.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156533.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
PA (AREN-) ARENA PHARM INC.
XX Behan DP, Lehmann-Brunisma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI: 2000-317986/27.
DR N-PSDB; AAA46031.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents
XX Example 1; Page 104-105; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably

XX A G-protein coupled 7 transmembrane receptor (AXOR-1).

DE Human: G-protein coupled seven transmembrane receptor; AXOR-1; infection;
 XX HIV-1; HIV-2; cancer; diabetes; obesity; anorexia; bulimia; asthma;
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 KW stroke; ulcer; asthma; allergy; benign prostatic hypertrophy; migraine;
 KW vomiting; psychotic disorder; neurological disorder; dyskinesia.

XX Homo sapiens.

OS
 XX
 PN MO9955734-A1.

XX
 PD 04-NOV-1999.

XX
 PF 20-APR-1999; 99WO-US08605.

XX
 PR 24-APR-1998; 98US-0082981.
 PR 17-JUN-1998; 98US-0089639.
 PR 16-FEB-1999; 99US-0251373.

XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
 PI Bergsma D, Elshourbagy N, Shabon U;

XX
 DR WPI; 2000-116269/10.

XX
 DR N-PSDB; AA245608.

PT Novel G-protein coupled transmembrane receptor for use in the treatment
 PT and diagnosis of diseases such as diabetes and Parkinson's disease -
 PS Claim 1; Page 26; 40pp; English.

XX
 XX The present sequence represents a human G-protein coupled seven
 CC transmembrane receptor designated AXOR-1. The AXOR-1 polypeptide is
 CC used for diagnosing disease. It is also used for identifying agonists
 CC and antagonists. The AXOR-1 polynucleotide, polypeptide, agonists and
 CC antagonists can be used to treat conditions such as bacterial, fungal,
 CC viral infections, particularly HIV-1 or 2, cancers, diabetes, obesity,
 CC anorexia, bulimia, asthma, Parkinson's disease, acute heart failure,
 CC hypotension, hypertension, urinary retention, osteoporosis, angina
 CC pectoris, myocardial infarction, stroke, ulcers, asthma, allergies,
 CC benign prostatic hypertrophy, migraine, vomiting, psychotic,
 CC neurological disorders and dyskinesias. The AXOR-1 polypeptide can also
 CC be used as an immunogen to produce immunospecific antibodies and to
 CC produce an immunological response.

XX
 SO Sequence 370 AA;

Query Match 100.0%; Score 1963; DB 21; Length 370;
 Best Local Similarity 100.0%; Pred. No. 2e-208;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANTSHADNLTQNLSPFLAFKLTSLGFIIGSVVGNLISLLVKKTLRAAYFEL 60
 DB 1 manyshaadnlqnlspflafkltslgfiigsvvgnllsllyvkktlhrayfll 60

QY 61 DLCCSDILRSACIPFPFNSTKYNSTWYTGTLTKVIAFLGLVSCFHFAMFICISVTRY 120
 DB 61 dlccsdilrsacipfpfnstknstwytglttkvialflglvscfhfaimfcisvtry 120

QY 121 LATAHFFYKRLTFWTCCLAVICWMTLSVMAAPPVLDVGTYSFIREDDCTQHRSEFR 180
 DB 121 latahffykrltfwtcclavicmwltlsvmaapppvldvgtysfireddctqhrsfr 180

QY 181 ANDSLGFMALLALLATOLVYLKLIFFVHDKRKRPVQFVAASQNTFFGPGASGQAA 240
 DB 181 andslgfmallalllatolvylkliffvhdrrkmpqfvaasqntffgpgasgaa 240

QY 241 ANMLAGRGRTPTPLTIGIQONANTGRRRLVLDERFMEKRISRMFYIMTFLFLTLMGP 300
 DB 241 anmlagrgrtptpltlgigqonantgrrrlvlderrfmeKRISRMFYIMTFLFLTLMGP 300

DB 241 anwlaagfgrgptlllgilqnanltgrrrlvlidelfmekrisrmfymtflfltlwgp 300

QY 301 YLVACYRWVFARGFVYEGFETAAVWMSFAOAGINPEFCISNRELRCSFTLLCYCKRS 360
 DB 301 ylvacyrwvfargfvyegfetaavwmsfagaqinpfvcilsnrelrcsfcllyckrs 360

QY 361 RLPREPYCVI 370
 DB 361 rlppepycvi 370

RESULT 7
 AAB73558
 ID AAB73558 standard; Protein: 370 AA.
 XX
 AC AAB73558;
 XX
 DT 07-AUG-2001 (first entry)
 XX
 DE Human GP27-like G protein-coupled receptor HE8N124.

XX
 KW HE8N124: GP27-like G protein-coupled receptor; 7TM receptor;
 KW infection; viral; bacterial; fungal; protozoan; HIV-1;
 KW HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia;
 KW osteoporosis; asthma; allergy; urinary retention;
 KW acute heart failure; hypotension; hypertension; angina pectoris;
 KW myocardial infarction; stroke; ulcer; migraine; vomiting;
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KW manic depression; bipolar disorder; depression; delirium; dementia;
 KW severe mental retardation; dyskinesia; Parkinson's disease;
 KW Huntington's disease; Gilles de la Tourette's syndrome; gene therapy;
 KW vaccine; drug screening; signal transduction.

XX
 OS Homo sapiens.

XX
 XX WO200132865-A1.
 XX
 PN 10-MAY-2001.
 PD
 XX 26-OCT-2000; 2000MO-BE10565.
 PF
 XX 03-NOV-1999; 99EP-0121785.
 PR
 XX (MERE) MERCK PATENT GMBH.
 PA
 PI Kluxen F;
 XX
 XX WPI; 2001-343484/36.
 DR N-PSDB; AAH23853.

PT Novel GP27-like polypeptide, HE8N124, useful for treating diseases
 PT involving microbial infections, cancers, obesity, asthma, diabetes,
 PT hypotension, osteoporosis, myocardial infarction, Parkinson's disease
 PT
 XX
 XX Claim 3; Page 42; 45pp; English.

XX
 PS The invention relates to the human GP27-like G protein-coupled receptor
 XX HE8N124 (AAB73558), to cDNA encoding HE8N124 (AAH23853), and to HE8N124
 CC fragments and variants. Like all G protein-coupled receptors, HE8N124
 CC has 7 putative transmembrane domains and is involved in signal
 CC transduction. HE8N124 was found to be expressed in brain, heart atria,
 CC spleen, lung, placenta, bladder and testis. The invention also relates
 CC to recombinant expression of HE8N124, and to an HE8N124-specific
 CC antibody. HE8N124 proteins and nucleotides may be used to treat a wide
 CC variety of disorders including bacterial, fungal, protozoal and viral
 CC infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign
 CC prostatic hypertrophy; diabetes; obesity; anorexia; bulimia;
 CC osteoporosis; asthma; allergies; urinary retention; acute heart failure;
 CC hypotension; hypertension; angina pectoris; myocardial infarction;
 CC stroke; migraine; ulcers; vomiting; psychotic and neurological disorders
 CC such as anxiety, schizophrenia, manic depression, depression, delirium,

CC neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile
CC dementia. The invention also provides genetic screening procedures that
CC entail analysing a person's genome with respect to GPCR. The vectors are
CC useful for the recombinant production of the GPCR's. The present sequence
CC is human CON202 G protein-coupled receptor (GPCR) protein.
XX
SQ Sequence 370 AA:

Query Match 100.0%; Score 1963; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e-208;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNLSPITAFKLTSLGFTIGSVGNLISITLVYDKTHRAPYELL 60
DB 1 manyshadniiqnlspitafkltslgftigsvgnlislilvdkthrapyyell 60
QY 61 DICCSDLISALCFPEFVNSVKNSTWYGTLCNKVIAFLGVLSCEFTAFELFCISVTRY 120
DB 61 diccsdlisalcfpfsvnsvknstwtgltcnkviaflgvlsceftafelfcisvtry 120
QY 121 LAIAHREFTKRLTEWTCLAVICMWTLSVAMAPPVLDVGVTSFIREDOCTFQHSFR 180
DB 121 laiahreftkrltewtclavicmwltlsvamappvldvgvtsfiredoctfqsfr 180
QY 181 ANDSIGEMLLALILATOLVYIKLIFVDRKRMKRVQVYAASQMTHTGPGASGOA 240
DB 181 andsigemllalilatolvylklifvdrkrmkrvqvyaasqmthtgpgasgoa 240
QY 241 ANWLAFGRGPPTLLIGIQONANTGRRLVLDEKMKRISRMVYIMTFELTLMP 300
DB 241 anwlagrgpptlligiqonantgrrlvldekkmkrismvyimtfeltlmp 300
QY 301 YLVACYWRVAFARQPVVGGFLTAQVMSFAQAGINPVCIFSNELRCFSTLLYCRKS 360
DB 301 ylvacywrvarfqpvvggfltaqvmsfaqaginpvcifsnelrcfstlllycrks 360
QY 361 RUPREYCVI 370
DB 361 rlpreycvi 370

RESULT 9

AAM99955 standard; Protein; 379 AA.

XX AAM99955;

XX 04-JAN-2002 (first entry)

XX Human expressed polypeptide SEQ ID NO 79.

XX Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX antiparkinsonian; antischizolng; antidiabetic; antithrilltic; cancer;
XX antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

XX WO20015387-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-0501310.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231245.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234987.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236337.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.

13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249269.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-465573/50.
 DR N-PSDB; AAI99567.
 XX
 PT Isolated digestive system associated polypeptide for treating,
 PT preventing and/or proposing disorders related to the digestive system
 PT including digestive system cancers and also for testing and detection
 PT e.g. diagnosis -
 XX
 PS Claim 11; SEQ ID NO 79; 509pp + Sequence Listing; English.
 XX

CC The invention relates to novel genes (AAI99548-AAI99604) and proteins
 CC (AAI99596-AAI99964) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published-pct-sequences.
 CC
 XX
 SQ Sequence 379 AA;
 Query Match 100.0%; Score 1963; DB 22; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2,1e-208;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1. MANYSHAADNIIONLSPFLAFLKLTSLGFLIGSVVGNLLISILVKKDTLHRAPIYFL 60
 DB 10 manyshaadnllgnlspflaflkltsgfligsvvgnllisilvkkdthrapyll 69
 QY 61 DCCSDILRSALICFPFVNSVKNKSTWYGTLCVKYIAELGVLSCHTAPMLFCISVTRY 120
 DB 70 dccsdilrsalicfpfvnsvknkstwygtlcvkyiaelgvlschthapmlfcisvtry 129
 QY 121 LAIAHREFTKRLTFWTCLAVICMWTLSVAMFPVLDVGTSTFIREDQCFQHSR 180
 DB 130 laiahreftkrltfwtclavicmwtlsvamfpvldvgtstfireedqcfqhsr 189
 QY 181 ANDSLGFMILLALILATOLVLYKLIFVHRRKMKPVQFAVSONMTPHGGASGOAA 240
 DB 190 andslgfmllalilatolvlyklifvhdrrkmkpvqfvaavsonmtpghgagaa 249
 QY 241 ANWLAFGFGPPPTLLGIRONANTGRRRLVLDKFKKRRISRMFYIMTFELTLMGP 300
 DB 250 anwlagfgpfpptllgirnntgrrllvldfkfkkrrisrmfymtftlmgp 309
 QY 301 YLVACTWRVPAKGPVYVGGELTAAVMSFRQAGINPVCIFSNRELRKCFSTLLCRKS 360
 DB 310 ylvactwrvpdkgpvyvvggeltaavmsfrqaginpvcifsnreldrkcftstllycrks 369
 QY 361 RLPREPYCVI 370
 DB 370 rlppepycvi 379
 RESULT 10
 AAB68873
 ID AAB68873 standard; Protein; 370 AA.
 AC AAB68873;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human RECAP polypeptide, SEQ ID NO: 3.
 XX
 KW Human; RECAP; receptors and associated proteins; cerebroprotective;
 KW neurotrophic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV;
 KW antidiabetic; immunostimulant; immunomodulator; antiinflammatory;
 KW antithyroid; immunosuppressive; nephrotoxic; antitumor; thyromimetic;
 KW cytostatic; antibacterial; virucide; fungicide; protozoacide;
 KW antileukosclerotic; hepatotropic; gene therapy; infection; cancer.
 KW
 OS Homo sapiens.

XX WO200107612-A2.
 PN
 XX
 XX 01-FEB-2001.
 PD
 XX
 XX 21-JUL-2000; 2000WO-US20035.
 PF
 XX
 XX 21-JUL-1999; 99US-0145232.
 PR 07-OCT-1999; 99US-0158578.
 PR 12-NOV-1999; 99US-0165192.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Au-Young J, Bandman O, Tang YT, Yue H, Azimzai Y, Burford N;
 PI Baughn MR, Lu DM, Hillman JL, Patterson C, Lal P;
 PI
 XX WPI: 2001-168554/17.
 DR N-PSDB; AAF58597.
 DR
 XX
 PT Novel receptors and associated proteins for diagnosis and treatment of
 PT neurological disorders, immunological disorders including autoimmune/
 PT inflammatory disorders and cell proliferative disorders such as cancer
 PT
 XX
 PS Claim 1; Page 96; 128pp; English.
 PS
 CC The present sequence is a human RECAP (receptors and associated
 CC proteins) polypeptide. RECAP polynucleotides and polypeptides are useful
 CC in the diagnosis, treatment and prevention of neurological disorders
 CC such as stroke, Alzheimer's disease, Pick's disease, Huntington's
 CC disease, dementia, Parkinson's disease, Down's syndrome, amyotrophic
 CC lateral sclerosis, multiple sclerosis, bacterial and viral meningitis,
 CC CJD (Creutzfeldt-Jakob disease), GSS (Gerstmann-Strausler-Scheinker
 CC syndrome), immunological disorders, including autoimmune/inflammatory
 CC disorders such as AIDS, Digeorge's syndrome, severe combined
 CC immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's
 CC disease, Addison's disease, autoimmune thyroiditis, Crohn's disease,
 CC diabetes mellitus, good pasture's syndrome, gout, Grave's diseases,
 CC Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral,
 CC bacterial, fungal, parasitic, protozoal, and helminthic infections; and
 CC cell proliferation disorders such as arteriosclerosis, atherosclerosis,
 CC cirrhosis, hepatitis and cancer.
 CC
 XX
 SO Sequence 370 AA.

Query Match 99.8%; Score 1959; DB 22; Length 370;
 Best Local Similarity 99.7%; Pred. No. 5.5e-208;
 Matches 369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MANYSHADNITQNTSPLTAFKLTSLGFIIGSVVGNLLISILVKKTKTLHAPYFELL 60
 DB 1 manyshadnltqntspltaflkltslgfiigsvvgnllisilvkkdktlhrapyfll 60
 OY 61 DDCGSDILRSATCFPEVENSNGSWTGTCTCKYIAFLGVLSCHTAFMLCISVTRY 120
 DB 61 ddcgsdiltarsatcfpevnsngswtgytclckyaiaflgvlschtlamlticstvy 120
 OY 121 LAIAHREFTKRLTEWTCIAVICMWTLSVAMAFPPVLVGTYSFIREDOCTFOHRSR 180
 DB 121 laiahreftkrltewtciavicmwtlsvamafpvvlvgtysfiredoctfohrrsr 180
 OY 181 ANDSGFMILLALILATOLVYIKLIEFVHRRKMKPVQFAVASQNWTFHGGASGQA 240
 DB 181 andsgfmillalilatlqlylkliffvdrtrkmpqvfavaeqnwtfhggasgqa 240
 OY 241 ANMLAGFGGPPPTLLIGROMANTGRRRLVLDFFKHEKRSKRFYIMTFPLLMGP 300
 DB 241 anmlagfggppptlligrnantgrrllvldffkhekrskrfyimtffllmwp 300
 OY 301 YLVACYWRFAFGPVVGGFLTAAVWMSFAQAGINPFCIFSNRELRCFSTLLYCRKS 360
 DB 301 ylvacywrfafgpvpvggfltaavwmsfaqaginpfcifsnrelrcfstlllycrks 360

OY 361 RLPREPCVI 370
 DB 361 rlprepcvi 370

RESULT 11
 AAY71300
 ID AAY71300 standard; Protein: 373 AA.
 XX
 XX AAY71300;
 AC
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Human orphan G protein-coupled receptor hARE-2.
 XX
 KW Human: orphan G protein-coupled receptor; GPCR; hARE-2; drug screening;
 KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
 XX
 OS Homo sapiens.
 XX
 PN WO200031258-A2.
 PD
 PD 02-JUN-2000.
 XX
 PF 13-OCT-1999; 99WO-US23687.
 XX
 PR 20-NOV-1998; 98US-0109213.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123949.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0136567.
 PR 28-MAY-1999; 99US-0137131.
 PR 28-MAY-1999; 99US-0141448.
 PR 29-JUN-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156634.
 PR 29-SEP-1999; 99US-0156653.
 PR 01-OCT-1999; 99US-0157280.
 PR 01-OCT-1999; 99US-0157281.
 PR 01-OCT-1999; 99US-0157282.
 PR 01-OCT-1999; 99US-0157293.
 PR 01-OCT-1999; 99US-0157294.
 PR 12-OCT-1999; 99US-0416760.
 PR 12-OCT-1999; 99US-0417044.
 XX
 PA (AREN-) ARENA PHARM INC.
 PI
 PI Chen R, Dang HT, Llaw CW, Lin I;
 DR
 DR WPI: 2000-40068/34.
 DR N-PSDB; AAD01127.
 XX

Novel human orphan G protein-coupled receptors and the encoding cDNAs
 for use in the identification of G protein-coupled receptor agonists -
 Claim 38; Page 67-68; 102pp; English.

The present amino acid sequence is the hARE-2, an endogenous human
 orphan G protein-coupled receptor (GPCR), expressed in the left and
 right cerebellum. The hARE-2 cDNA was identified using ESTs (expressed
 sequence tag) A1090920 and 68530 as a probe.
 The orphan GPCR of the invention, like all GPCRs has seven transmembrane
 C-terminal. However, no endogenous ligands has yet been identified for
 the proteins of the invention. The orphan GPCRs may be used in the
 identification of their endogenous ligands, and to screen potential GPCR
 agonists and antagonists for use as pharmaceutical agents. The proteins

PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.

QY 358 --RKSRLPREPYCVI 370

358 --RKSRLPREPYCVI 370

| Accession | Protein | Species | Length | Score | E-value | Identity | Positives | Gaps | Conserved Domains |
|-----------|---------------------------------------------------------------------------|-----------------------------------------------------------------|--------|-------|---------|----------|-----------|------|-------------------|
| QY | 1 | MANTSHADNLQNLSR--LNAFLKTLNLSGFIIGVSVVGNLLISILVKKOTLHRAAPYF | 58 | | | | | | |
| Db | 1 | manttgepeevsgalspsasaaykvllvllgilmcvsIagualllslvlkeralkkapyf | 60 | | | | | | |
| OY | 59 | LLDLCSDSILKSAICFPFVFNKNGSTWTGTCTCKVIAFLVGLSCFHAFMLCISVT | 118 | | | | | | |
| Db | 61 | llldlcadgtrtsavcfrpvlasyvghsgwtlsalscklvaafmalfcfhaafmlfcisvt | 120 | | | | | | |
| OY | 119 | RYLAIAHHRFYTKRLTFWTCLAVICWVTLSSVAMAFPPVLVDVGTYSFIREDOCTFOHS | 178 | | | | | | |
| Db | 121 | rymalahrfyfakrmclwtlcaavlcwawtlsvamafrpvtfdvgtykfifreeqclifehry | 180 | | | | | | |
| OY | 179 | FRANDSGCFMILLILLILALPOLVLTCLKILFPHDRKKKKKPOFVAASONTFPGSGG | 238 | | | | | | |
| Db | 181 | fkancltglmflmlavlnaahavvgkllllfeyrhrkmkpvqmpaalsqntvflngpaga | 240 | | | | | | |
| OY | 239 | AAANLAFGCGRPPEPTLGRONANNTGRRLLVLDFEFKKERKISIMFELPFTLW | 298 | | | | | | |
| Db | 241 | aaanvtaagfygypmpelllgtrqghaas-trllgmdevygeklgymfaifallllllw | 299 | | | | | | |
| OY | 299 | GPYLVACTYRWVFPANGPVVGGFLTAWVMSFAQAGINPEVCISFSNRELRCFST--TLLY | 356 | | | | | | |
| Db | 300 | spylavcywrfvfkacavphrylatawvmsfagaavpivcfllnkdllkcltrhapcw | 359 | | | | | | |
| OY | 357 | CRKSLRPREPYCVI | 370 | | | | | | |
| Db | 360 | tggapaprepycvm | 373 | | | | | | |
| RESULT 15 | | | | | | | | | |
| AAM99953 | | | | | | | | | |
| ID | AAM99953 standard; Protein: 378 AA. | | | | | | | | |
| XX | AAM99953; | | | | | | | | |
| AC | 04-JAN-2002 (first entry) | | | | | | | | |
| DE | Human expressed polypeptide SFO ID NO 77. | | | | | | | | |
| XX | Human; nocotropic; neuroprotective; cytostatic; dermatological; virucide; | | | | | | | | |
| KW | immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary; | | | | | | | | |
| KW | antiparkinsonian; antisclothing; antihaemic; antiallergic; cancer; | | | | | | | | |
| KW | antirheumatic; hepatotropic; cerebrotropic; antinflammatory; | | | | | | | | |
| KW | antiallergic; antidiabetic; antilicer; anticonvulsant; antifungal; | | | | | | | | |
| KW | antiarasitic; cardiac; immune disorder; cardiovascular disorder; | | | | | | | | |
| KW | neurological disease; infection; nephrotropic; gene therapy; vaccine. | | | | | | | | |
| XX | Homo sapiens. | | | | | | | | |
| OS | Wo200155387-A1. | | | | | | | | |
| PN | 02-AUG-2001. | | | | | | | | |
| XX | 17-JAN-2001; 2001WO-US01310. | | | | | | | | |
| PD | 31-JAN-2000; 2000US-0179065. | | | | | | | | |
| XX | 04-FEB-2000; 2000US-0180622. | | | | | | | | |
| PR | 24-FEB-2000; 2000US-0184664. | | | | | | | | |
| PR | 02-MAR-2000; 2000US-0186350. | | | | | | | | |
| PR | 16-MAR-2000; 2000US-0189874. | | | | | | | | |
| PR | 17-MAR-2000; 2000US-0190076. | | | | | | | | |

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|----|-------------|----------------|
| PR | 15-JUN-2000 | 200005-0220966 |
| PR | 14-AUG-2000 | 200005-0224518 |
| PR | 14-AUG-2000 | 200005-0224518 |
| PR | 14-AUG-2000 | 200005-0225213 |
| PR | 14-AUG-2000 | 200005-0225214 |
| PR | 14-AUG-2000 | 200005-0225266 |
| PR | 14-AUG-2000 | 200005-0225267 |
| PR | 14-AUG-2000 | 200005-0225268 |
| PR | 14-AUG-2000 | 200005-0225279 |
| PR | 14-AUG-2000 | 200005-0225270 |
| PR | 14-AUG-2000 | 200005-0225447 |
| PR | 14-AUG-2000 | 200005-0225757 |
| PR | 14-AUG-2000 | 200005-0225758 |
| PR | 23-AUG-2000 | 200005-0226929 |
| PR | 30-AUG-2000 | 200005-0228924 |
| PR | 01-SEP-2000 | 200005-0228287 |
| PR | 01-SEP-2000 | 200005-0229343 |
| PR | 01-SEP-2000 | 200005-0229344 |
| PR | 01-SEP-2000 | 200005-0229345 |
| PR | 05-SEP-2000 | 200005-0229513 |
| PR | 05-SEP-2000 | 200005-0229519 |
| PR | 06-SEP-2000 | 200005-0230437 |
| PR | 06-SEP-2000 | 200005-0230438 |
| PR | 08-SEP-2000 | 200005-0231242 |
| PR | 08-SEP-2000 | 200005-0231243 |
| PR | 08-SEP-2000 | 200005-0231244 |
| PR | 08-SEP-2000 | 200005-0231413 |
| PR | 08-SEP-2000 | 200005-0231414 |
| PR | 08-SEP-2000 | 200005-0233080 |
| PR | 08-SEP-2000 | 200005-0233081 |
| PR | 12-SEP-2000 | 200005-0233968 |
| PR | 14-SEP-2000 | 200005-0233997 |
| PR | 14-SEP-2000 | 200005-0233998 |
| PR | 14-SEP-2000 | 200005-0234223 |
| PR | 21-SEP-2000 | 200005-0234225 |
| PR | 21-SEP-2000 | 200005-0234274 |
| PR | 25-SEP-2000 | 200005-0234997 |
| PR | 25-SEP-2000 | 200005-0234998 |
| PR | 26-SEP-2000 | 200005-0235484 |
| PR | 27-SEP-2000 | 200005-0235834 |
| PR | 27-SEP-2000 | 200005-0235836 |
| PR | 27-SEP-2000 | 200005-0235837 |
| PR | 29-SEP-2000 | 200005-0236367 |
| PR | 29-SEP-2000 | 200005-0236368 |
| PR | 29-SEP-2000 | 200005-0236369 |
| PR | 29-SEP-2000 | 200005-0236370 |
| PR | 02-OCT-2000 | 200005-0237032 |
| PR | 02-OCT-2000 | 200005-0237033 |
| PR | 02-OCT-2000 | 200005-0237037 |
| PR | 02-OCT-2000 | 200005-0237039 |
| PR | 02-OCT-2000 | 200005-0237040 |
| PR | 13-OCT-2000 | 200005-0239335 |
| PR | 13-OCT-2000 | 200005-0239397 |
| PR | 20-OCT-2000 | 200005-0240960 |
| PR | 20-OCT-2000 | 200005-0241121 |
| PR | 20-OCT-2000 | 200005-0241785 |
| PR | 20-OCT-2000 | 200005-0241786 |
| PR | 20-OCT-2000 | 200005-0241787 |
| PR | 20-OCT-2000 | 200005-0241808 |
| PR | 20-OCT-2000 | 200005-0241809 |
| PR | 20-OCT-2000 | 200005-0241826 |
| PR | 01-NOV-2000 | 200005-0244617 |
| PR | 08-NOV-2000 | 200005-0245474 |
| PR | 08-NOV-2000 | 200005-0246475 |

